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OM protein - protein search, using sw model

Run on: May 20, 2005, 13:22:17 ; Search time 42 Seconds
(without alignments)
1050.419 Million cell updates/sec

Title: US-10-659-549-3
Perfect score: 3043
Sequence: 1 MALEIHMSDPMCLTENFNEQ.....GEARSCGQGWQKVVV 591

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pap:*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pap:*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pap:*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pap:*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3043	100.0	591	4	US-09-643-657-3
2	2610.5	85.8	633	2	US-08-736-770-3
3	1966.5	64.6	605	4	US-09-949-016-8823
4	1958.5	64.4	592	2	US-08-736-770-6
5	1958.5	64.4	592	4	US-09-702-705-1809
6	1958.5	64.4	592	4	US-09-736-457-1809
7	1958.5	64.4	592	4	US-09-643-657-4
8	1958.5	64.4	592	4	US-09-671-325-1809
9	1897	62.3	591	2	US-08-736-770-5
10	1897	62.3	591	4	US-09-643-657-5
11	1881	61.8	608	2	US-08-736-770-1
12	1832.5	60.2	583	4	US-09-949-016-8267
13	1765.5	58.0	589	4	US-09-643-657-14
14	1757.5	57.8	591	4	US-09-643-657-15
15	1459.5	48.0	620	4	US-09-643-657-13
16	932.5	30.6	573	4	US-09-643-657-18
17	526	17.3	147	4	US-09-370-838-99
18	526	17.3	147	4	US-09-854-133-99
19	509	16.7	159	4	US-09-370-838-98
20	509	16.7	159	4	US-09-854-133-98
21	392	12.9	96	4	US-09-513-999C-5037
22	296	9.7	103	4	US-09-643-657-16
23	239	7.9	64	4	US-09-643-657-17
24	203	6.7	57	4	US-09-621-976-4483
25	197	6.5	573	4	US-09-270-767-4491
26	154.5	5.0	1427	4	US-09-538-092-1044
27	151	5.0	1180	4	US-09-543-681A-6436

28	148	4.9	710	4	US-09-107-532A-5067	Sequence 5067, Ap
29	148	4.9	1288	4	US-09-919-039-209	Sequence 209, App
30	146.5	4.8	1531	4	US-09-418-710-29	Sequence 29, Appl
31	146.5	4.8	1531	4	US-09-839-479-29	Sequence 29, Appl
32	145.5	4.8	568	4	US-09-949-016-10580	Sequence 10580, A
33	144	4.7	1857	4	US-09-917-254-91	Sequence 91, Appl
34	144	4.7	1972	4	US-09-538-092-1084	Sequence 1084, Ap
35	144	4.7	1984	4	US-09-949-016-7111	Sequence 7111, Ap
36	144	4.7	1984	4	US-09-949-016-7112	Sequence 7112, Ap
37	144	4.7	1984	4	US-09-949-016-7113	Sequence 7113, Ap
38	142	4.7	1972	4	US-08-875-435B-4	Sequence 4, Appli
39	141.5	4.7	1527	4	US-09-418-710-27	Sequence 27, Appl
40	141.5	4.7	1527	4	US-09-839-479-27	Sequence 27, Appl
41	140.5	4.6	897	1	US-08-095-737-4	Sequence 4, Appli
42	140.5	4.6	897	2	US-08-480-145-4	Sequence 4, Appli
43	140.5	4.6	897	2	US-08-477-389-4	Sequence 4, Appli
44	140.5	4.6	1540	4	US-09-949-016-7037	Sequence 7037, Ap
45	140.5	4.6	2107	4	US-09-949-016-7646	Sequence 7646, Ap

ALIGNMENTS

RESULT 1
US-09-643-657-3
; Sequence 3, Application US/09643657
; Patent No. 6642024
; GENERAL INFORMATION:
; APPLICANT: Diane Pennica
; TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,657
; FILING DATE: 17-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,089A
; FILING DATE: 29-Jan-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1056
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-643-657-3

Query Match 100.0%; Score 3043; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.7e-254;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEIHMSDPMCLTENFNEQLEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
Db 1 MALEIHMSDPMCLTENFNEQLEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60

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QY 61 KKGFSVASTVQSHTKGIWICVPHNPNHNTLVLLDTEGLGDEKADNKNDIQIFALAL 120
DB 61 KKGFSVASTVQSHTKGIWICVPHNPNHNTLVLLDTEGLGDEKADNKNDIQIFALAL 120
QY 121 LLSSTFVYNTVTKIDQGAIDLHNVTELTDLKARNSPDLDRVEDPADSASFFPDVWTL 180
DB 121 LLSSTFVYNTVTKIDQGAIDLHNVTELTDLKARNSPDLDRVEDPADSASFFPDVWTL 180
QY 181 RPFCLGLEIDGQLVTPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCFIFDLPA 240
DB 181 RPFCLGLEIDGQLVTPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCFIFDLPA 240
QY 241 HQKLAQLLETLPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVITYN 300
DB 241 HQKLAQLLETLPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVITYN 300
QY 301 AISSGDLPCIEENAVLALAQRENSAAVOKAIAHYDQMGQKQVLPMETLQELLDLHRTSER 360
DB 301 AISSGDLPCIEENAVLALAQRENSAAVOKAIAHYDQMGQKQVLPMETLQELLDLHRTSER 360
QY 361 EAIEVFMKNSFKDQVDSFOKELETLDAKQNDICKRNLEASSDYCSALLKDIKFGPLEEAV 420
DB 361 EAIEVFMKNSFKDQVDSFOKELETLDAKQNDICKRNLEASSDYCSALLKDIKFGPLEEAV 420
QY 421 KQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVQLQKYLKSKESVSHAILQTDQAL 480
DB 421 KQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVQLQKYLKSKESVSHAILQTDQAL 480
QY 481 TETETKKEAQAQVKAEEKAEQAQRLAAIORQNEQMMQERLHQEQVQMEIAKQNWLAQ 540
DB 481 TETETKKEAQAQVKAEEKAEQAQRLAAIORQNEQMMQERLHQEQVQMEIAKQNWLAQ 540
QY 541 QKQMOEQMVFNCFISPLPVTMRVCSGKEGEAARSCSGSQGQVWSQKVMV 591
DB 541 QKQMOEQMVFNCFISPLPVTMRVCSGKEGEAARSCSGSQGQVWSQKVMV 591
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RESULT 2

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US-08-736-770-3
; Sequence 3, Application US/08736770
; Patent No. 5871965
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN GUANYLATE BINDING PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/736,770
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0145 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 633 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-08-736-770-3
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Query Match 85.8%; Score 2610.5; DB 2; Length 633;
Best Local Similarity 94.4%; Pred. No. 4.8e-217;
Matches 519; Conservative 8; Mismatches 20; Indels 3; Gaps 3;

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QY 1 MALEIHMSDPMCLIEFNELQKVNQEBALISAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
DB 1 MALEIHMSDPMCLIEFNELQKVNQEBALISAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
QY 61 KKGFSVASTVQSHTKGIWICVPHNPNHNTLVLLDTEGLGDEKADNKNDIQIFALAL 120
DB 61 KKGFSVASTVQSHTKGIWICVPHNPNHNTLVLLDTEGLGDEKADNKNDIQIFALAL 118
QY 121 LLSSTFVYNTVTKIDQGAIDLHNVTELTDLKARNSPDLDRVEDPADSASFFPDVWTL 180
DB 119 LLSSTFVYNTVTKIDQGAIDLHNVTELTDLKARNSPDLDRVEDPADSASFFPDVWTL 178
QY 181 RPFCLGLEIDGQLVTPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCFIFDLPA 239
DB 179 KDFCLGLEIDGQLVTPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCFIFDLPA 238
QY 240 AHQKLAQLLETLPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVITY 299
DB 239 AHQKLAQLLETLPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVITY 298
QY 300 NAISSGDLPCIEENAVLALAQRENSAAVOKAIAHYDQMGQKQVLPMETLQELLDLHRTSE 359
DB 299 NAISSGDLPCIEENAVLALAQRENSAAVOKAIAHYDQMGQKQVLPMETLQELLDLHRTSE 358
QY 360 REAIEVFMKNSFKDQVDSFOKELETLDAKQNDICKRNLEASSDYCSALLKDIKFGPLEEA 419
DB 359 REAIEVFMKNSFKDQVDSFOKELETLDAKQNDICKRNLEASSDYCSALLKDIKFGPLEEA 418
QY 420 VKQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVQLQKYLKSKESVSHAILQTDQ 479
DB 419 VKQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVQLQKYLKSKESVSHAILQTDQ 478
QY 480 LTETETKKEAQAQVKAEEKAEQAQRLAAIORQNEQMMQERLHQEQVQMEIAKQNWLA 539
DB 479 LTETETKKEAQAQVKAEEKAEQAQRLAAIORQNEQMMQERLHQEQVQMEIAKQNWLA 538
QY 540 QKQMOEQMVFNCFISPLPVTMRVCSGKEGEAARSCSGSQGQVWSQKVMV 591
DB 539 QKQMOEQMVFNCFISPLPVTMRVCSGKEGEAARSCSGSQGQVWSQKVMV 591
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RESULT 3

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US-09-949-016-8823
; Sequence 8823, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8823
/ LENGTH: 605
/ TYPE: PRT
/ ORGANISM: Human
/ US-09-949-016-8823

Query Match      64.6%; Score 1966.5; DB 4; Length 605;
Best Local Similarity 69.7%; Pred. No. 2.2e-161;
Matches 389; Conservative 70; Mismatches 88; Indels 11; Gaps 3;

QY 1 MALEHMSDPMCLINENFNEOLKVNQAEALILSAITQPVVVVAIVGLYRTGKSYLNNKLAG 60
Db 14 MASEIHMTGPMCLIENTNGRLMANPEALKILSAITQPMVVVAIVGLYRTGKSYLNNKLAG 73
QY 61 KKGFSVASTVQSHTKGIWCVPHNPWPHHTLVLLDTEGLGDEKADNKNDIQIPALAL 120
Db 74 KKGFSVASTVQSHTKGIWCVPHNPWPHHTLVLLDTEGLGDEKADNKNDSWIFALAV 133
QY 121 LLSSTFVYNTVTKIDQGAIDLLHNVTETDLLKARNSPD--LDRVEDPADSASFPPDLVW 178
Db 134 LLSSTFVYNTVTKIDQGAIDLLHNVTETDLLKARNSPD--LDRVEDPADSASFPPDLVW 178
QY 179 TLRFCLGLEIDGQVTPDEYLFNSLRPKQSDQVQNFNLPRLCIQKFFPKKCFVDFR 238
Db 194 TLRFCLGLEIDGQVTPDEYLFNSLRPKQSDQVQNFNLPRLCIQKFFPKKCFVDFR 253
QY 239 PAHQKLAQLETLPDDELEPEFVQVTFPCSYIFSHSMTKTLPGGIMVNGSLKMLVLT 298
Db 254 PVHRRKLAQLETLPDDELEPEFVQVTFPCSYIFSHSMTKTLPGGIMVNGSLKMLVLT 313
QY 299 VNAISSGDLPCINAVLAQRENSAAVQKAIHAHYDQMGQKQVQLPMTLQELLDLHRTS 358
Db 314 VNAISSGDLPCINAVLAQRENSAAVQKAIHAHYDQMGQKQVQLPMTLQELLDLHRTS 373
QY 359 EREAIEVFMKNSFKVDQSFQKLETLDDAKQNDICRKNLEASSDYCSALLKIDFGPLEE 418
Db 374 EREAIEVFMKNSFKVDQSFQKLETLDDAKQNDICRKNLEASSDYCSALLKIDFGPLEE 433
QY 419 AVKQGIYSKPGGNYLFIQTEELKAKYRPRKGIQAEVQLQKYLKSKESVSHAILQTDQ 478
Db 434 EVKAGIYSKPGGNYLFIQTEELKAKYRPRKGIQAEVQLQKYLKSKESVSHAILQTDQ 493
QY 479 ALTETEKKKKAQVKAABAKAORLAAIQRQNEQMOERERLHQEQVQ-----MEIAQ 534
Db 494 TLTEKEKEIEVERVKAESAQASAKMLQENQKQMEQKERSYQEHKQLTKERMENDRV 553
QY 535 NWLAQQ-----KMQEQQ 547
Db 554 QLLKEQERTLALKQEQE 571

RESULT 4
US-08-736-770-6
/ Sequence 6, Application US/08736770
/ Patent No. 5871965
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Au-Young, Janice
/ APPLICANT: Hillman, Jennifer L.
/ TITLE OF INVENTION: NOVEL HUMAN GUANYLATE BINDING PROTEINS
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: US
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
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/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/736,770
/ FILING DATE: Filed Herewith
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PP-0145 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 592 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 183002
/ US-08-736-770-6

Query Match      64.4%; Score 1958.5; DB 2; Length 592;
Best Local Similarity 69.4%; Pred. No. 1.1e-160;
Matches 387; Conservative 71; Mismatches 89; Indels 11; Gaps 3;

QY 1 MALEHMSDPMCLINENFNEOLKVNQAEALILSAITQPVVVVAIVGLYRTGKSYLNNKLAG 60
Db 1 MASEIHMTGPMCLIENTNGRLMANPEALKILSAITQPMVVVAIVGLYRTGKSYLNNKLAG 60
QY 61 KKGFSVASTVQSHTKGIWCVPHNPWPHHTLVLLDTEGLGDEKADNKNDIQIPALAL 120
Db 61 KKGFSVASTVQSHTKGIWCVPHNPWPHHTLVLLDTEGLGDEKADNKNDSWIFALAV 120
QY 121 LLSSTFVYNTVTKIDQGAIDLLHNVTETDLLKARNSPD--LDRVEDPADSASFPPDLVW 178
Db 121 LLSSTFVYNTVTKIDQGAIDLLHNVTETDLLKARNSPD--LDRVEDPADSASFPPDLVW 180
QY 179 TLRFCLGLEIDGQVTPDEYLFNSLRPKQSDQVQNFNLPRLCIQKFFPKKCFVDFR 238
Db 181 TLRFCLGLEIDGQVTPDEYLFNSLRPKQSDQVQNFNLPRLCIQKFFPKKCFVDFR 240
QY 239 PAHQKLAQLETLPDDELEPEFVQVTFPCSYIFSHSMTKTLPGGIMVNGSLKMLVLT 298
Db 241 PVHRRKLAQLETLPDDELEPEFVQVTFPCSYIFSHSMTKTLPGGIMVNGSLKMLVLT 300
QY 299 VNAISSGDLPCINAVLAQRENSAAVQKAIHAHYDQMGQKQVQLPMTLQELLDLHRTS 358
Db 301 VNAISSGDLPCINAVLAQRENSAAVQKAIHAHYDQMGQKQVQLPMTLQELLDLHRTS 360
QY 359 EREAIEVFMKNSFKVDQSFQKLETLDDAKQNDICRKNLEASSDYCSALLKIDFGPLEE 418
Db 361 EREAIEVFMKNSFKVDQSFQKLETLDDAKQNDICRKNLEASSDYCSALLKIDFGPLEE 420
QY 419 AVKQGIYSKPGGNYLFIQTEELKAKYRPRKGIQAEVQLQKYLKSKESVSHAILQTDQ 478
Db 421 EVKAGIYSKPGGNYLFIQTEELKAKYRPRKGIQAEVQLQKYLKSKESVSHAILQTDQ 480
QY 479 ALTETEKKKKAQVKAABAKAORLAAIQRQNEQMOERERLHQEQVQ-----MEIAQ 534
Db 481 TLTEKEKEIEVERVKAESAQASAKMLQENQKQMEQKERSYQEHKQLTKERMENDRV 540
QY 535 NWLAQQ-----KMQEQQ 547
Db 541 QLLKEQERTLALKQEQE 558

RESULT 5
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US-09-702-705-1809
; Sequence 1809, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1809
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-702-705-1809

Query Match 64.4%; Score 1958.5; DB 4; Length 592;
Best Local Similarity 69.4%; Pred. No. 1.1e-160;
Matches 387; Conservative 71; Mismatches 89; Indels 11; Gaps 3;

Qy 1 MALEIHMSDPMCLINFNQKLVQAEILSAITQPVVVVAIVGLYRTGKSYLMNKL 60
Db 1 MASEIHTGPMCLIENTNGLMANPEALKILSAITQPMVVVAIVGLYRTGKSYLMNKL 60

Qy 61 KNGFSVASTVQSHYKGIWCVPHNPWNTLVLLDTGEGDVEKADNKNDIOIFALAL 120
Db 61 KKGFGSLGTVQSHYKGIWCVPHNPWNTLVLLDTGEGDVEKADNKNDIOIFALAL 120

Qy 121 LLSSTFVYNTVANKIDOGAIDLLHNVTETLTLKARNSPD--LDRVEDPADSFPDVLV 178
Db 121 LLSSTFVYNSIGTINQAMDQLYYVTELTHIRSKSSPDENENEVEDSADFVSFPDFV 180

Qy 179 TLDRFCGLGIDQLVTPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCFIPDL 238
Db 181 TLDRFSLDLADGQPLTPDEYLTSLKKGTSQKDETFNLPRLCIRKFFPKKCFVDR 240

Qy 239 PAHQKLAQLETLPPDELEPEFVQVTEFCSVIFSHSMTKTLPGGIMVNGSLKNLVLT 298
Db 241 PVHRRKLAQLEKLQDELDPEFVQVADFCSVIFSNKTKTLSSGQVNGPRLESVLTY 300

Qy 299 VNAISSGDLPCINAVIALAORENSAAVOKATAHYDQMGOKVQVLPMTLOELDLHRTS 358
Db 301 VNAISSGDLPCMENAVIALAORENSAAVOKATAHYEQMGOKVQVLPMTLOELDLHRTS 360

Qy 359 ERAIEVFMKNSFKVDQSFQKELETLLDAKNDICRNLKLEASSDYCSALLKDI FGPLEE 418
Db 361 ERAIEVFISSFKVDVHLFQKELAAQLEKKEDDFCKQNEASSDRCSGLLQVIFSPLEE 420

Qy 419 AVKQGISYKPGGHNLFTQKTEELKAKYREPRKGIQAEVLQKYLKSKESVSHAILQTDQ 478
Db 421 EVKAGIYSKPGGYRLVFQKLQDLKKYYEPRKGIQAEVILQYLKSKESMTDAILOTDQ 480

Qy 479 ALTETEKKEAQAQKAEKAEQALAAIQORNEQMGQERLHQEVRO----MEIAKQ 534
Db 481 TLTEKEKEIEVERVKAESAQASAKMLQEMQRKNEQMEQKERSYOEHLKQLTERKENDRV 540

Qy 535 NWLAEEQ-----KMQEQQ 547
Db 541 QLLKEQERTIALKLEQEQ 558

RESULT 6
US-09-736-457-1809
; Sequence 1809, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1809
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-1809

Query Match 64.4%; Score 1958.5; DB 4; Length 592;
Best Local Similarity 69.4%; Pred. No. 1.1e-160;
Matches 387; Conservative 71; Mismatches 89; Indels 11; Gaps 3;

Qy 1 MALEIHMSDPMCLINFNQKLVQAEILSAITQPVVVVAIVGLYRTGKSYLMNKL 60
Db 1 MASEIHTGPMCLIENTNGLMANPEALKILSAITQPMVVVAIVGLYRTGKSYLMNKL 60

Qy 61 KNGFSVASTVQSHYKGIWCVPHNPWNTLVLLDTGEGDVEKADNKNDIOIFALAL 120
Db 61 KKGFGSLGTVQSHYKGIWCVPHNPWNTLVLLDTGEGDVEKADNKNDIOIFALAL 120

Qy 121 LLSSTFVYNTVANKIDOGAIDLLHNVTETLTLKARNSPD--LDRVEDPADSFPDVLV 178
Db 121 LLSSTFVYNSIGTINQAMDQLYYVTELTHIRSKSSPDENENEVEDSADFVSFPDFV 180

Qy 179 TLDRFCGLGIDQLVTPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCFIPDL 238
Db 181 TLDRFSLDLADGQPLTPDEYLTSLKKGTSQKDETFNLPRLCIRKFFPKKCFVDR 240

Qy 239 PAHQKLAQLETLPPDELEPEFVQVTEFCSVIFSHSMTKTLPGGIMVNGSLKNLVLT 298
Db 241 PVHRRKLAQLEKLQDELDPEFVQVADFCSVIFSNKTKTLSSGQVNGPRLESVLTY 300

Qy 299 VNAISSGDLPCINAVIALAORENSAAVOKATAHYDQMGOKVQVLPMTLOELDLHRTS 358
Db 301 VNAISSGDLPCMENAVIALAORENSAAVOKATAHYEQMGOKVQVLPMTLOELDLHRTS 360

Qy 359 ERAIEVFMKNSFKVDQSFQKELETLLDAKNDICRNLKLEASSDYCSALLKDI FGPLEE 418
Db 361 ERAIEVFISSFKVDVHLFQKELAAQLEKKEDDFCKQNEASSDRCSGLLQVIFSPLEE 420

Qy 419 AVKQGISYKPGGHNLFTQKTEELKAKYREPRKGIQAEVLQKYLKSKESVSHAILQTDQ 478
Db 421 EVKAGIYSKPGGYRLVFQKLQDLKKYYEPRKGIQAEVILQYLKSKESMTDAILOTDQ 480

Qy 479 ALTETEKKEAQAQKAEKAEQALAAIQORNEQMGQERLHQEVRO----MEIAKQ 534
Db 481 TLTEKEKEIEVERVKAESAQASAKMLQEMQRKNEQMEQKERSYOEHLKQLTERKENDRV 540

Qy 535 NWLAEEQ-----KMQEQQ 547
Db 541 QLLKEQERTIALKLEQEQ 558

RESULT 7
US-09-643-657--4

```

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; Sequence 4, Application US/09643657
; Patent No. 6642024
; GENERAL INFORMATION:
; APPLICANT: Diane Pennica
; TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,657
; FILING DATE: 17-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,089A
; FILING DATE: 29-Jan-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1056
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/425-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 592 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-643-657-4

Query Match 64.4%; Score 1958.5; DB 4; Length 592;
Best Local Similarity 69.4%; Pred. No. 1.1e-160;
Matches 387; Conservative 71; Mismatches 89; Indels 11; Gaps 3;

Qy 1 MALEHMSDPMCLIEFNBNQKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
Db 1 MASEIHTGPMCLIENTNGLMANPEALKILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
Qy 61 KNGKFSVASTVQSHTKGIWVCVPHPNWPNHTLVLLDTEGLGDVEKADKNNDIQIFALAL 120
Db 61 KKGKFSLSGTVQSHTKGIWVCVPHPKPGHILVLLDTEGLGDVEKADKNNDISWIFALAV 120
Qy 121 LLSSTFVYNTVKNIDOGAIDLLHNVTETLLKARNSPD--LDRVEDPADSASFPFDLVW 178
Db 121 LLSSTFVYNSIGTINQAMQDLYVYVTELTTHRIRSKSSPDENENEVEDSADFSVFPDFVW 180
Qy 179 TLRFDFCLGLEIDQVLTPEYLENSLRPKQSDQVQNFNLPRLCICQKFFPKKCFIFDL 238
Db 181 TLRFDSLLEADGQPLTPDEYLTVSLKKGTSQKDETFNLPRLCIRKFFPKKCFVDR 240
Qy 239 PAHQKKLAQLETLPDDELPPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLLKVLVITY 298
Db 241 PVHRRKLAQLEKLQDELDPEFVQVADFCSYIFSNSKTKTLGGIQVNGPRLESVLITY 300
Qy 299 VNAISSGDLPCENAVLALAQRENSAAVOKAIAHYDQMGQKQVLPMTLOELDLHRTS 358
Db 301 VNAISSGDLPCMENAVLALAQIENSAAVOKAIAHYEQMGQKQVLPMTLESQELDLHRTS 360
Qy 359 EREAIEVFMKNSFKVDQSFQKELETLLDAKNDICRNLKASSDYCSALLKDIFFGLEE 418
Db 361 EREAIEVIRSFKVDVHLPFKELAQAQLEKKRDRDFCKQNEASSDRCSGLLQVIFSPLEE 420
Qy 419 AVKQGIYSKPGGHNLFIQKTEELKAKYRPREPKGIQAEEVLQKYLKSKESVSHAILQTDQ 478

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Db 421 EVKAGIYSGGVRFLVQKLDLKKYIEPRKGIQABEILQTLKSKESMTDAILLQTDQ 480
QY 479 ALTETKKKKAQVKAABAEKAEORLAATQORNEQMMQERLHQEVQRQ----MEIAKQ 534
Db 481 TLTEKEKEIEVERKVAESAQAASAKMLQEMQKNEQMMQEKERSYQSHLKQLTKERMENDRV 540
QY 535 NWLAEOQ-----KMQEQQ 547
Db 541 QLLKEQERTLALKLQEQE 558

RESULT 9

US-08-736-770-5
; Sequence 5, Application US/08736770
; Patent No. 5871965
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN GUANYLATE BINDING PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/736,770
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0145 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 829177
US-08-736-770-5

Query Match 62.3%; Score 1897; DB 2; Length 591;
Best Local Similarity 63.5%; Pred. No. 2.2e-155;
Matches 377; Conservative 88; Mismatches 101; Indels 28; Gaps 4;

QY 1 MALEIHMSDPMCLIEFNQELKVNQEALETLSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
Db 1 MAPEINLPGMSLIDNTKGOLVNVPEALKILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
QY 61 KNGKFSVASTVQSHTKGIMTWCPHPNPNHTLVLLDTEGLGDPVEKADNKNDIQIFALAL 120
Db 61 KNGKFSVASTVQSHTKGIMTWCPHPNPNHTLVLLDTEGLGDPVEKADNKNDIQIFALAI 120
QY 121 LLSSTFVYNTVNVKIDQGAIDLLHNVTBLTDLKARNSPDLDRVEDPADSASFFPDLVWTL 180
Db 121 LLSSTFVYNSMGTINGQAMDQLHVVTBLTDLKARNSPGNSVDDSDADPVSPFPFVWTL 180

QY 181 RDFCLGLEIDGOLVTPDEYLENSLRPKGSDORVONFNLPRLCIOKFFPKKCKFIEDLPA 240
Db 181 RDTTLEVDGPGPITADDYLELSLKURGTDKKSKSFNDPRLCIRKFFPKKCFVFDWEA 240
QY 241 HOKKLAQETLTPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVWNGSRLKNLVLYVN 300
Db 241 PKKYLALHLEQLKEEELNPDFIEQVAEFCSYILSHSNVKTLSGGIAVNGPRLESVLVLYVN 300
QY 301 AISSGDLPCINAVIALAQRENSAAVQKAIHYDQMGOKVQLPMETLQELDLHRTSER 360
Db 301 AISSGDLPCMENAVIALAQIENSAAVEKAIHYEQMGOKVQLPTETLQELDLHRTSER 360
QY 361 EALEVFMKNSFKVDVDSFOKELETLLDAKNDICKENLEASDYCSALIKDIFGPLEEAV 420
Db 361 EALEVFMKNSFKVDVDMFORKIGLALEARDDFCQNSKASSDCCMALLQDIFGPLEEDV 420
QY 421 KQGIYSKPGGHNLFQKTEELKAKYVREPRKGIQABEVLQKYLKSKESVSHAILQTDQAL 480
Db 421 KQGTFSKPGGYRLFTQKLELKNKYQVPRKGIQAKEVLKYLESKEDVADALLQTDQSL 480
QY 481 TETEKKKKAQVKAABAEKAEORLAATQORNEQMMQERLHQEVQRQ----MEIAKQNW 536
Db 481 SEKERAIEVERIKAESAESAALKMLEIEIKKNEBMMQEKESYQEHVKQLTKERMDRAQL 540
QY 537 LAEQ-----KMQEQQMVFINCFISPLPVTMRVCSGKGEAARSCGSOQGVW 585
Db 541 MAEQEKTALKLQEQE-----RLKKEGFENESKR---LQKDIW 575

RESULT 10

US-09-643-657-5
; Sequence 5, Application US/09643657
; Patent No. 6642024
; GENERAL INFORMATION:
; APPLICANT: Diane Pennica
; TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,657
FILING DATE: 17-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/015,089A
FILING DATE: 29-Jan-1998
ATTORNEY/AGENT INFORMATION:
NAME: Hasek, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1056
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-643-657-5

Query Match 62.3%; Score 1897; DB 4; Length 591;

Best Local Similarity 63.5%; Pred. No. 2.2e-155;
Matches 377; Conservative 88; Mismatches 101; Indels 28; Gaps 4;
QY 1 MALEIHMSDPMLCIENFNEQKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLNKLAG 60
DB 1 MAPEINLPGLMSLIDNTKQGVVNEALKILSAITQPVVVVAIVGLYRTGKSYLNKLAG 60
QY 61 KNGFSVASTVQSHTKGIWICVPHNPNTLVLDDTEGLDVEKADKNDIQIFALAL 120
DB 61 KNGFSLAGTSKSHTKGIWICVPHNPNTLVLDDTEGLDVEKADKNDIQIFALAL 120
QY 121 LLSSTFVNTVNTKIDQGAIDLHNVTETLLKARNSPDLRVEDPADSASFFPDLVTL 180
DB 121 LLSSTFVNTVNTKIDQGAIDLHNVTETLLKARNSPDLRVEDPADSASFFPDLVTL 180
QY 181 RDCFLGLEIDQLVTPDEYLENSLRPKGSDORVQNFNLPRLCIOKFFPKKCFIDPLA 240
DB 181 RDCFLGLEIDQLVTPDEYLENSLRPKGSDORVQNFNLPRLCIOKFFPKKCFIDPLA 240
QY 241 HOKLAQLETLDPDELEPFVQVTEFCYSYIFSHSMTKLPGGIMVNGSRKLNVLTVN 300
DB 241 PKYLAHLEQLKEELNPDFFIEQVAEFCYSYILSHSNVKTLSGGIAVNGPRLESVLTVN 300
QY 301 AISSGDLPCENAVLALAQIENSAAVKAIAHYEQMGQKQVLPPTETLQELLDLHRDSE 360
DB 301 AISSGDLPCENAVLALAQIENSAAVKAIAHYEQMGQKQVLPPTETLQELLDLHRDSE 360
QY 361 EAIEVFMKNSFKVDQSFQKLETLDAKNDICRNLEASDDYCSALLKIDIFGLPBEAV 420
DB 361 EAIEVFMKNSFKVDQSFQKLETLDAKNDICRNLEASDDYCSALLKIDIFGLPBEAV 420
QY 421 KQGIYKPGGHNLFIOKTEELKAKYRPRKGIQAEVLQKYLKESVSHAILQTDQAL 480
DB 421 KQGIYKPGGHNLFIOKTEELKAKYRPRKGIQAEVLQKYLKESVSHAILQTDQAL 480
QY 481 TETEKKEAQAQVKAIAEAEKAEQRLAAIQORNEQMMQERLHQBQVQVQVQVQVQV 536
DB 481 SEKEKAIEVERIKAEAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAE 540
QY 537 LAEQQ-----KMQEQMQVFCISPLPVMRVSCSGEAEARSQSGQGVW 585
DB 541 MAEQKTLALQEQE-----RLKKEGFENESKR---LQKDIW 575

RESULT 11

US-08-736-770-1
; Sequence 1, Application US/08736770
; Patent No. 5871965
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN GUANYLATE BINDING PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/736,770
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0145 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4186
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 608 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-08-736-770-1
Query Match 61.8%; Score 1881; DB 2; Length 608;
Best Local Similarity 66.0%; Pred. No. 5.6e-154;
Matches 372; Conservative 78; Mismatches 104; Indels 10; Gaps 3;
QY 1 MALEIHMSDPMLCIENFNEQKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLNKLAG 60
DB 1 MALEIHMSDPMLCIENFNEQKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLNKLAG 60
QY 61 KNGFSVASTVQSHTKGIWICVPHNPNTLVLDDTEGLDVEKADKNDIQIFALAL 120
DB 61 KNGFSVASTVQSHTKGIWICVPHNPNTLVLDDTEGLDVEKADKNDIQIFALAL 120
QY 121 LLSSTFVNTVNTKIDQGAIDLHNVTETLLKARNSPDLRVEDPADSASFFPDLVTL 180
DB 121 LLSSTFVNTVNTKIDQGAIDLHNVTETLLKARNSPDLRVEDPADSASFFPDLVTL 180
QY 181 RDCFLGLEIDQLVTPDEYLENSLRPKGSDORVQNFNLPRLCIOKFFPKKCFIDPLA 240
DB 181 RDCFLGLEIDQLVTPDEYLENSLRPKGSDORVQNFNLPRLCIOKFFPKKCFIDPLA 240
QY 241 HOKLAQLETLDPDELEPFVQVTEFCYSYIFSHSMTKLPGGIMVNGSRKLNVLTVN 299
DB 241 KXKYLXLEQLKEELNPDFFIEQVAEFCYSYILSHSNVKTLSGGIAVNGPRLESVLTVN 300
QY 300 NAISGDLPCENAVLALAQIENSAAVKAIAHYEQMGQKQVLPPTETLQELLDLHRDSE 359
DB 300 NAISGDLPCENAVLALAQIENSAAVKAIAHYEQMGQKQVLPPTETLQELLDLHRDSE 360
QY 360 REAIEVFMKNSFKVDQSFQKLETLDAKNDICRNLEASDDYCSALLKIDIFGLPBEA 419
DB 360 REAIEVFMKNSFKVDQSFQKLETLDAKNDICRNLEASDDYCSALLKIDIFGLPBEA 420
QY 420 KQGIYKPGGHNLFIOKTEELKAKYRPRKGIQAEVLQKYLKESVSHAILQTDQAL 479
DB 420 KQGIYKPGGHNLFIOKTEELKAKYRPRKGIQAEVLQKYLKESVSHAILQTDQAL 480
QY 480 LTETEKKEAQAQVKAIAEAEKAEQRLAAIQORNEQMMQERLHQBQVQVQVQVQVQV 535
DB 480 LSEKEKAIEVERIKAEAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAE 540
QY 536 WLAEQQ-----KMQEQMQVFCISPLPVMRVSCSGEAEARSQSGQGVW 554
DB 541 LMEQKTLALQEQE-----RLKKEGFENESKR---LQKDIW 564

RESULT 12

US-09-949-016-8267
; Sequence 8267, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016

/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8267
/ LENGTH: 583
/ TYPE: PRT
/ ORGANISM: Human
/ US-09-949-016-8267

Query Match 60.2%; Score 1832.5; DB 4; Length 583;
Best Local Similarity 66.2%; Pred. No. 8.2e-150;
Matches 366; Conservative 65; Mismatches 91; Indels 31; Gaps 2;

QY 1 MALEIHMSDPMCLINFNQKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
DB MAPEIHMTGPMCLIENTNGLVANPEALKILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 117

QY 61 KNGKFSVASTVQSHTKGIWICVPHNPNHNTLVLLDTEGLGDKVEKADNKNDIQIFALAL 120
DB 118 KNGKFSLSGTVSKHTKGIWMCVPHPKPEHTLVLLDTEGLGDKVKKQNDNSWIFTLAV 177

QY 121 LLSSTFVYNTVVKIDQGAIDLHNVTETDLKARNSPDLDRVEDPADSASFPDDLVTWL 180
DB 178 LLSSTLVYNSMGTINQQAAMDQLYVVTETLTHIRSKSPDENENEDSADFVSFPDFVWTL 237

QY 181 RPFCLGLEIDGQVTPDEYLENSLRPKQSDORVQNFNLPRLCIQKFFPKKCFIFDLPA 240
DB 238 RDFSLEADGQPLTPDEYLEVSLKLTQGTQSKDKNFNLPRLCIRKFFPKKCFVFDLPI 297

QY 241 HOKKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLVTYVN 300
DB 298 HRRKLAQLEKLDDELDPEFVQVADFCSYIFSNKTKLSGGIKVNGPRLSLVLYTN 357

QY 301 AISSGDLPCIEANAVLALAQRENSAAVQKAIADHYDQMGQKQVLPMTTLOELDLHRTSR 360
DB 358 AISRGDLPCMENAVLALAQIENSAAVQKAIADHYDQMGQKQVLPMTTLOELDLHRAQ-- 415

QY 361 EAIEVPMKNSFKDVQDSFOKELETLDAKNDICKENLEASSDYCSALLKDIKDFPLEEAV 420
DB 416 -----LDKRRDDFCQKQNEASSDRCSALLQVIFSPDEEEV 450

QY 421 KOGIYKPGGHNLFIOKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
DB 451 KAGIYKPGGYCLFIQKLDLEKKYEEPRKGIQAEVILQYLYKSKESVTDAILQTDQIL 510

QY 481 TETETKKKKAQVKAEEAKAEQRLAAIQRQNEQMQRERLHQEQVRQ-----MEIAKQNW 536
DB 511 TEKEKEIEVCVKAESAQAKMVEBNQIKYQOMMEBEKESYQEHVKQLTEKMERERAQL 570

QY 537 LAFQKQKMQEQMQ 549
DB 571 LEEQEKLTLSKLQ 583

RESULT 13
US-09-643-657-14
/ Sequence 14, Application US/09643657
/ Patent No. 6642024
/ GENERAL INFORMATION:
/ APPLICANT: Diane Pennica
/ TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
/ NUMBER OF SEQUENCES: 43
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California

/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/643,657
/ FILING DATE: 17-Aug-2000
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/015,089A
/ FILING DATE: 29-Jan-1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Haseak, Janet E.
/ REGISTRATION NUMBER: 28,616
/ REFERENCE/DOCKET NUMBER: P1056
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-1896
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 589 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-643-657-14

Query Match 58.0%; Score 1765.5; DB 4; Length 589;
Best Local Similarity 61.7%; Pred. No. 5.2e-144;
Matches 343; Conservative 95; Mismatches 109; Indels 9; Gaps 2;

QY 1 MALEIHMSDPMCLINFNQKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
DB 1 MASEIHMSPEMCLIENTEAQLVINOEARLSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60

QY 61 KNGKFSVASTVQSHTKGIWICVPHNPNHNTLVLLDTEGLGDKVEKADNKNDIQIFALAL 120
DB 61 KRTGFSLSGTVQSHTKGIWMCVPHPKKAGOTLVLLDTEGLGDKVEKADNKNDIQIFALAV 120

QY 121 LLSSTFVYNTVVKIDQGAIDLHNVTETDLKARNSPDLDRVEDPADSASFPDDLVTWL 180
DB 121 LLSSTFIYNSIGTINQQAAMDQLYVVTETLTHIRSKSPDENENEDSADFVSFPDFVWTL 180

QY 181 RPFCLGLEIDGQVTPDEYLENSLRPKQSDORVQNFNLPRLCIQKFFPKKCFIFDLPA 240
DB 181 RDFSLEADGQPLTPDEYLEVSLKLTQGTQSKDKNFNLPRLCIRKFFPKKCFIFDRPG 240

QY 241 HOKKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLVTYVN 300
DB 241 DRKQSLKSWIQEDQKNEFVQVADFCSYIFSGVKTLSGGITVNGPRLSLVLYTVS 300

QY 301 AISSGDLPCIEANAVLALAQRENSAAVQKAIADHYDQMGQKQVLPMTTLOELDLHRTSR 360
DB 301 AICSGELPCMENAVLTLAQIENSAAVQKAITTYEQMNQKIHMPTETLQELDLHRTCR 360

QY 361 EAIEVPMKNSFKDVQDSFOKELETLDAKNDICKENLEASSDYCSALLKDIKDFPLEEAV 420
DB 361 EAIEVPMKNSFKDVQDSFOKELETLDAKNDICKENLEASSDYCSALLKDIKDFPLEEAV 420

QY 421 KOGIYKPGGHNLFIOKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
DB 421 KOGTFYKPGGYLFLQKQLEKKYLOTPGKGLQAEVMLRKYPESKEDLADTLKNDQSL 480

QY 481 TETETKKKKAQVKAEEAKAEQRLAAIQRQNEQMQRERLHQEQVRQ-----MEIAKQNW 536
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QY 537 LAFQKQKMQEQMQ 547
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RESULT 14
US-09-643-657-15
; Sequence 15, Application US/09643657
; Patent No. 6642024
; GENERAL INFORMATION:
; APPLICANT: Diane Pennica
; TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,657
; FILING DATE: 17-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,089A
; FILING DATE: 29-Jan-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1056
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-643-657-15
Query Match 57.8%; Score 1459.5; DB 4; Length 591;
Best Local Similarity 63.3%; Pred. No. 2.6e-143;
Matches 346; Conservative 82; Mismatches 116; Indels 3; Gaps 1;
Qy 1 MALETHSDPMCLIFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLNNKLAG 60
Db 3 MASEHMLQPMCLIENTEAHLVINOEALEILSAINQPVVVAIVGLYRTGKSYLNNKLAG 62
Qy 61 KNKGSVASTVQSHTKGIWICVPHNPNTLVLLDTGEGLDVEKADKNNDIOIFALAL 120
Db 63 KRTGSLSTVQSHTKGIWICVPHNPNTLVLLDTGEGLDVEKADKNNDIOIFALAL 122
Qy 121 LLSSTFVYNTVKNIDQGAIDLHNVTETLLKARNSPDLDRVEDPADSASFFPDVWTL 180
Db 123 LLSSTFVYNTVKNIDQGAIDLHNVTETLLKARNSPDLDRVEDPADSASFFPDVWTL 182
Qy 181 RDFCLGLIDQLVTPDYLNSLPKGSQORVONFNLPLCTOKPFPKCKCFIDPLA 240
Db 183 RDFSLELVNGKLVTPDYLNSLPKGSQORVONFNLPLCTOKPFPKCKCFIDPLA 242
Qy 241 HOKLAQLETPDDLEPEFVQVTEFCYSIFSHSMTKTLPGLMVNGSLKLNVLTVYN 300
Db 243 LRKQCKLETIGEELCESEFVEQVAEFTSYIFSYSAVTKLGGIIVNGPRKLSLVQTVG 302
Qy 301 AISSGDLPCIEAVLALAQRENSAAVQKAIAYHQDMQKQVQLPMETIQELLDLHRTSER 360
Db 303 AISSGSLFCMESAVLTLAQIENSAVQKAIAYHQDMQKQVQLPMETIQELLDLHRTSER 362
Qy 361 EAIEVFMQNSPKVDQSKFQETLLDQAKNDICRNLKAEASDVCSALLKIDIFGLEBAV 420
Db 363 EAIEVFMQNSPKVDQSKFQETLLDQAKNDICRNLKAEASDVCSALLKIDIFGLEBAV 422
Qy 421 KQGIYSKPGHNLFTQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
Db 423 KQGTSPKPGYFLFLQMEQLEKKYQAPGKGLAEAVLKKYFESKEDIVETLLKTDQSL 482
Qy 481 TETEKKKKEAQVKAFAEAQRLAAIQORNEQMMQOERLHQBQVQRMETAKQNWLABQ 540
Db 483 TEAAKEIEVERIKATBAEAAANRELAERKQKFTELAMQKKEESYQEHVRQL---TEKMKERQ 539
Qy 541 QKMOEQ 547
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RESULT 15
US-09-643-657-13
; Sequence 13, Application US/09643657
; Patent No. 6642024
; GENERAL INFORMATION:
; APPLICANT: Diane Pennica
; TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,657
; FILING DATE: 17-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,089A
; FILING DATE: 29-Jan-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1056
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 620 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-643-657-13
Query Match 48.0%; Score 1459.5; DB 4; Length 620;
Best Local Similarity 51.2%; Pred. No. 1.6e-117;
Matches 281; Conservative 118; Mismatches 145; Indels 5; Gaps 2;
Qy 7 MSDPMCLIFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLNNKLAGNKQGS 66
Db 1 MEAPICLVENWKNQLTVNLLEAIRILEQIAQLVVAIVGLYRTGKSYLNNKLAGNHGFS 60
Qy 67 VASTVQSHTKGIWICVPHNPNTLVLLDTGEGLDVEKADKNNDIOIFALALLSSTF 126
Db 61 LGSTVQSETKGIWICVPHNPNTLVLLDTGEGLDVEKADKNNDIOIFALALLSSTF 120
Qy 127 VYNTVKNIDQGAIDLHNVTETLLKARNSPDLDRVEDPADSASFFPDVWTLRDFCLG 186
Db 121 VYNSMSTINQALBQLHFVTELTQLIRAKSPREDKVKDSSEFVGFPPDFIWAVERDALE 180
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 20, 2005, 13:29:02 ; Search time 136 Seconds
(without alignments)
1453.632 Million cell updates/sec

Title: US-10-659-549-3

Perfect score: 3043

Sequence: 1 MALETHMSDPMCLTIFNEQ.....GEARSCGQGVWSQKVV 591

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
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- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2815	92.5	586	14	US-10-028-072-46
2	2815	92.5	586	14	US-10-140-808-46
3	2815	92.5	586	14	US-10-121-049-46
4	2815	92.5	586	14	US-10-123-904-46
5	2815	92.5	586	14	US-10-140-470-46
6	2815	92.5	586	14	US-10-175-746-46
7	2815	92.5	586	14	US-10-176-918-46
8	2815	92.5	586	14	US-10-176-921-46
9	2815	92.5	586	14	US-10-137-865-46
10	2815	92.5	586	14	US-10-140-474-46
11	2815	92.5	586	14	US-10-142-431-46
12	2815	92.5	586	14	US-10-143-114-46
13	2815	92.5	586	14	US-10-142-419-46

14	2815	92.5	586	14	US-10-123-262-46
15	2815	92.5	586	14	US-10-142-423-46
16	2815	92.5	586	14	US-10-121-050-46
17	2815	92.5	586	14	US-10-141-755-46
18	2815	92.5	586	14	US-10-143-032-46
19	2815	92.5	586	14	US-10-123-108-46
20	2815	92.5	586	14	US-10-123-236-46
21	2815	92.5	586	14	US-10-123-261-46
22	2815	92.5	586	14	US-10-140-921-46
23	2815	92.5	586	14	US-10-140-928-46
24	2815	92.5	586	14	US-10-121-045-46
25	2815	92.5	586	14	US-10-123-282-46
26	2815	92.5	586	14	US-10-123-903-46
27	2815	92.5	586	14	US-10-124-822-46
28	2815	92.5	586	14	US-10-140-925-46
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45	2815	92.5	586	14	US-10-147-500-46

ALIGNMENTS

RESULT 1

US-10-028-072-46
; Sequence 46, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Deanovers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17


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; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

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Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MALEIHMSDPCLLENFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60

Qy 61 KNGFSVASTVQSHTKGIWICVPHNPNNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
Db 61 KNGFSVASTVQSHTKGIWICVPHNPNNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy 121 LLSSTFVYNTVTKIDQGAIDLLHNVTETDILLKARNSPDLDRVEDPADSASFFPDVWTL 180
Db 121 LLSSTFVYNTVTKIDQGAIDLLHNVTETDILLKARNSPDLDRVEDPADSASFFPDVWTL 180

Qy 181 RDFCLGLEIDQVTPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFPFKKCFIDPLA 240
Db 181 RDFCLGLEIDQVTPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFPFKKCFIDPLA 240

Qy 241 HOKKLAQLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYN 300
Db 241 HOKKLAQLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYN 300

Qy 301 AISSGDLPCIEENAVLALAORENSAAVQKAIHYDQMGOKVQLPMTLOELLDLHRTSER 360
Db 301 AISSGDLPCIEENAVLALAORENSAAVQKAIHYDQMGOKVQLPMTLOELLDLHRTSER 360

Qy 361 EAI EIVFMKNSPKVDQSFQKELETLLDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420
Db 361 EAI EIVFMKNSPKVDQSFQKELETLLDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420

Qy 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVLYQKYLKSKESVSHAILQTDQAL 480
Db 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVLYQKYLKSKESVSHAILQTDQAL 480

Qy 481 TETEKKKAEQVKAEEKAEKAEQRLAAIQRONEQMQRERLHQVQVROMETAKQNWLAEQ 540
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RESULT 2

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US-10-140-808-46
; Sequence 46, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen

```

```

; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140,808
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-808-46

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Query Match      92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEIHMSDPCLLENFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
Db 1 MALEIHMSDPCLLENFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60

Qy 61 KNGFSVASTVQSHTKGIWICVPHNPNNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
Db 61 KNGFSVASTVQSHTKGIWICVPHNPNNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

Qy 121 LLSSTFVYNTVTKIDQGAIDLLHNVTETDILLKARNSPDLDRVEDPADSASFFPDVWTL 180
Db 121 LLSSTFVYNTVTKIDQGAIDLLHNVTETDILLKARNSPDLDRVEDPADSASFFPDVWTL 180

Qy 181 RDFCLGLEIDQVTPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFPFKKCFIDPLA 240
Db 181 RDFCLGLEIDQVTPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFPFKKCFIDPLA 240

Qy 241 HOKKLAQLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYN 300
Db 241 HOKKLAQLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYN 300

Qy 301 AISSGDLPCIEENAVLALAORENSAAVQKAIHYDQMGOKVQLPMTLOELLDLHRTSER 360
Db 301 AISSGDLPCIEENAVLALAORENSAAVQKAIHYDQMGOKVQLPMTLOELLDLHRTSER 360

Qy 361 EAI EIVFMKNSPKVDQSFQKELETLLDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420
Db 361 EAI EIVFMKNSPKVDQSFQKELETLLDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420

Qy 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVLYQKYLKSKESVSHAILQTDQAL 480
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Qy 481 TETEKKKAEQVKAEEKAEKAEQRLAAIQRONEQMQRERLHQVQVROMETAKQNWLAEQ 540
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Db 541 QKMQEQQMQ 549

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; Sequence 46, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
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; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-46

Query Match          92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MALEIHMSDPMCLIEFNQKLVQAEILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
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DB 121 LLSSTFVYNTVANKIDOGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDDLVTWL 180
QY 181 RDFCLGLEIDGQLVTPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFFPKKCFIFDLPA 240
DB 181 RDFCLGLEIDGQLVTPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFFPKKCFIFDLPA 240
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DB 241 HQKLAQLETLDPDELEPEFVQVTFECSYIFSHSMTKTLPGGIMVNGSRLKNLVITYN 300
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DB 301 ATSSGDLPCIEAVLALAORENSAAVQKAIHYDQMGOKVOLPMETLQELLDLHRTSER 360
QY 361 EAIEVFMKNSFKVDQSFQKELETLDDAKNDICRNLKLEASSDYCSALLKIDIFGPLEEAV 420
DB 361 EAIEVFMKNSFKVDQSFQKELETLDDAKNDICRNLKLEASSDYCSALLKIDIFGPLEEAV 420
QY 421 KQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHALIQTDQAL 480
DB 421 KQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHALIQTDQAL 480
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RESULT 4
US-10-123-904-46
; Sequence 46, Application US/10123904
; Publication No. US2003002328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-46

Query Match          92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEIHMSDPMCLIEFNQKLVQAEILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
DB 1 MALEIHMSDPMCLIEFNQKLVQAEILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
QY 61 KKGFSVASTVQSHTKGIWICVPHNPNHNTLVLLDTGLGDEKADNNDIQIFALAL 120
DB 61 KKGFSVASTVQSHTKGIWICVPHNPNHNTLVLLDTGLGDEKADNNDIQIFALAL 120
QY 121 LLSSTFVYNTVANKIDOGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDDLVTWL 180
DB 121 LLSSTFVYNTVANKIDOGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDDLVTWL 180
QY 181 RDFCLGLEIDGQLVTPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFFPKKCFIFDLPA 240
DB 181 RDFCLGLEIDGQLVTPDEYLENSLRPKQSGDQVQNFNLPRLCIQKFFPKKCFIFDLPA 240
QY 241 HQKLAQLETLDPDELEPEFVQVTFECSYIFSHSMTKTLPGGIMVNGSRLKNLVITYN 300
DB 241 HQKLAQLETLDPDELEPEFVQVTFECSYIFSHSMTKTLPGGIMVNGSRLKNLVITYN 300
QY 301 ATSSGDLPCIEAVLALAORENSAAVQKAIHYDQMGOKVOLPMETLQELLDLHRTSER 360
DB 301 ATSSGDLPCIEAVLALAORENSAAVQKAIHYDQMGOKVOLPMETLQELLDLHRTSER 360
QY 361 EAIEVFMKNSFKVDQSFQKELETLDDAKNDICRNLKLEASSDYCSALLKIDIFGPLEEAV 420
DB 361 EAIEVFMKNSFKVDQSFQKELETLDDAKNDICRNLKLEASSDYCSALLKIDIFGPLEEAV 420
```

QY 421 KQIYKPGGHNLFQKTEELKAKYRPRKGIQAEVLUQYLYKSKESVSHAILQTDQAL 480
DB 421 KQIYKPGGHNLFQKTEELKAKYRPRKGIQAEVLUQYLYKSKESVSHAILQTDQAL 480
QY 481 TETEKKKKEAQVKAEAEKAEQRLAAIORQNEQMMQERERLHQBQVQRMETIAKQNWLABQ 540
DB 481 TETEKKKKEAQVKAEAEKAEQRLAAIORQNEQMMQERERLHQBQVQRMETIAKQNWLABQ 540
QY 541 QKMQEQQMQ 549
DB 541 QKMQEQQMQ 549
RESULT 5
US-10-140-470-46
; Sequence 46, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C150
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-46
Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALEIHMSPCLNENFNEQKVNQAELEILSAITQPVVVAIVGLYRTGKSYLANKLAG 60
DB 1 MALEIHMSPCLNENFNEQKVNQAELEILSAITQPVVVAIVGLYRTGKSYLANKLAG 60
QY 61 KNGKFSVASTVQSHTKGIWICVPHNPWPNHTLVLLDTTEGLGDVEKADKNDIQIFALAL 120
DB 61 KNGKFSVASTVQSHTKGIWICVPHNPWPNHTLVLLDTTEGLGDVEKADKNDIQIFALAL 120
QY 121 LLSSTFVYNTVKNIDQGAIDLHNVTELTDLKARNSPDLRVEDPADSASFFPDVWTL 180
DB 121 LLSSTFVYNTVKNIDQGAIDLHNVTELTDLKARNSPDLRVEDPADSASFFPDVWTL 180
QY 181 RDCFLGLEIDQGLVTPDPEYLENSLRPKQSGDQORVQNFNLPRLCIQKFFPKKCFIDLPA 240
DB 181 RDCFLGLEIDQGLVTPDPEYLENSLRPKQSGDQORVQNFNLPRLCIQKFFPKKCFIDLPA 240
QY 241 HOKKLAQLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLTVYN 300
DB 241 HOKKLAQLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLTVYN 300

QY 301 AISSGDLPCIEANVLALAQRENSAAVKAIAYHDOQMKGKQVLPMTLOELLDLHRTSR 360
DB 301 AISSGDLPCIEANVLALAQRENSAAVKAIAYHDOQMKGKQVLPMTLOELLDLHRTSR 360
QY 361 EAEIVFMKNSFKVDVDSFQKELETLLDAKNDICRNLKASDYCSALLKDIKFGPLEEAV 420
DB 361 EAEIVFMKNSFKVDVDSFQKELETLLDAKNDICRNLKASDYCSALLKDIKFGPLEEAV 420
QY 421 KQIYKPGGHNLFQKTEELKAKYRPRKGIQAEVLUQYLYKSKESVSHAILQTDQAL 480
DB 421 KQIYKPGGHNLFQKTEELKAKYRPRKGIQAEVLUQYLYKSKESVSHAILQTDQAL 480
QY 481 TETEKKKKEAQVKAEAEKAEQRLAAIORQNEQMMQERERLHQBQVQRMETIAKQNWLABQ 540
DB 481 TETEKKKKEAQVKAEAEKAEQRLAAIORQNEQMMQERERLHQBQVQRMETIAKQNWLABQ 540
QY 541 QKMQEQQMQ 549
DB 541 QKMQEQQMQ 549
RESULT 6
US-10-175-746-46
; Sequence 46, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-46
Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALEIHMSPCLNENFNEQKVNQAELEILSAITQPVVVAIVGLYRTGKSYLANKLAG 60
DB 1 MALEIHMSPCLNENFNEQKVNQAELEILSAITQPVVVAIVGLYRTGKSYLANKLAG 60
QY 61 KNGKFSVASTVQSHTKGIWICVPHNPWPNHTLVLLDTTEGLGDVEKADKNDIQIFALAL 120
DB 61 KNGKFSVASTVQSHTKGIWICVPHNPWPNHTLVLLDTTEGLGDVEKADKNDIQIFALAL 120
QY 121 LLSSTFVYNTVKNIDQGAIDLHNVTELTDLKARNSPDLRVEDPADSASFFPDVWTL 180
DB 121 LLSSTFVYNTVKNIDQGAIDLHNVTELTDLKARNSPDLRVEDPADSASFFPDVWTL 180
QY 181 RDCFLGLEIDQGLVTPDPEYLENSLRPKQSGDQORVQNFNLPRLCIQKFFPKKCFIDLPA 240


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Db      181  RDVCLGLDGLVTPDEYLENSLRPKQSGDQDVQNFNLPRLCIQKFFPKKCFIDLPA 240
QY      241  HQKLAQLETLPDDELEPEFVQVTEFCYSIFSHSMTKTLPGGIMVNGSRLKNLVLYYN 300
Db      241  HQKLAQLETLPDDELEPEFVQVTEFCYSIFSHSMTKTLPGGIMVNGSRLKNLVLYYN 300
QY      301  AISSGDLPCIEANVLALAQRENSAAVOKAIAHYDOOMGQKQVLPMETLOELDLHRTSER 360
Db      301  AISSGDLPCIEANVLALAQRENSAAVOKAIAHYDOOMGQKQVLPMETLOELDLHRTSER 360
QY      361  EAIEVFMKNSFKVDQSFQKELETLLDAKQNDICRNLKRNLEASDYCSALLKDIFGPLEEAV 420
Db      361  EAIEVFMKNSFKVDQSFQKELETLLDAKQNDICRNLKRNLEASDYCSALLKDIFGPLEEAV 420
QY      421  KQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQAL 480
Db      421  KQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQAL 480
QY      481  TETEKKKKAQVKAEEAKAEQRLAAIORQNEQMMQERERLHOEQVRQMEIAKQNWLAQ 540
Db      481  TETEKKKKAQVKAEEAKAEQRLAAIORQNEQMMQERERLHOEQVRQMEIAKQNWLAQ 540
QY      541  QXMQEQQMQ 549
Db      541  QXMQEQQMQ 549
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RESULT 7

US-10-176-918-46

; Sequence 46, Application US/10176918

; Publication No. US20030027275A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C382

; CURRENT APPLICATION NUMBER: US/10/176,918

; CURRENT FILING DATE: 2002-06-20

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 46

; LENGTH: 586

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-176-918-46

Query Match 92.5%; Score 2815; DB 14; Length 586;

Best Local Similarity 100.0%; Pred. No. 8.2e-197;

Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1  MALEIHMSDPMCLIEFNQKVNQEALETLSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
Db      1  MALEIHMSDPMCLIEFNQKVNQEALETLSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
QY      61  KNKGFSAVTSQSHTKGIWICVPHPNWPNHTLVLLDTGLGDEVKADNKNDIQIFALAL 120
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```
Db      61  KNKGFSAVTSQSHTKGIWICVPHPNWPNHTLVLLDTGLGDEVKADNKNDIQIFALAL 120
QY      121  LLSSTFVNTVNTKIDQGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFDPDLVMTL 180
Db      121  LLSSTFVNTVNTKIDQGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFDPDLVMTL 180
QY      181  RDVCLGLDGLVTPDEYLENSLRPKQSGDQDVQNFNLPRLCIQKFFPKKCFIDLPA 240
Db      181  RDVCLGLDGLVTPDEYLENSLRPKQSGDQDVQNFNLPRLCIQKFFPKKCFIDLPA 240
QY      241  HQKLAQLETLPDDELEPEFVQVTEFCYSIFSHSMTKTLPGGIMVNGSRLKNLVLYYN 300
Db      241  HQKLAQLETLPDDELEPEFVQVTEFCYSIFSHSMTKTLPGGIMVNGSRLKNLVLYYN 300
QY      301  AISSGDLPCIEANVLALAQRENSAAVOKAIAHYDOOMGQKQVLPMETLOELDLHRTSER 360
Db      301  AISSGDLPCIEANVLALAQRENSAAVOKAIAHYDOOMGQKQVLPMETLOELDLHRTSER 360
QY      361  EAIEVFMKNSFKVDQSFQKELETLLDAKQNDICRNLKRNLEASDYCSALLKDIFGPLEEAV 420
Db      361  EAIEVFMKNSFKVDQSFQKELETLLDAKQNDICRNLKRNLEASDYCSALLKDIFGPLEEAV 420
QY      421  KQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQAL 480
Db      421  KQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVVLQKYLKSKESVSHAILQTDQAL 480
QY      481  TETEKKKKAQVKAEEAKAEQRLAAIORQNEQMMQERERLHOEQVRQMEIAKQNWLAQ 540
Db      481  TETEKKKKAQVKAEEAKAEQRLAAIORQNEQMMQERERLHOEQVRQMEIAKQNWLAQ 540
QY      541  QXMQEQQMQ 549
Db      541  QXMQEQQMQ 549
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RESULT 8

US-10-176-921-46

; Sequence 46, Application US/10176921

; Publication No. US20030027276A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C288

; CURRENT APPLICATION NUMBER: US/10/176,921

; CURRENT FILING DATE: 2002-06-20

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 46

; LENGTH: 586

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-176-921-46

Query Match 92.5%; Score 2815; DB 14; Length 586;

Best Local Similarity 100.0%; Pred. No. 8.2e-197;

Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 1 MALEIHMSDPMCLIFNFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLKNKLAG 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 61 KNGKFSVASTVQSHTKGIIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 61 KNGKFSVASTVQSHTKGIIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 121 LLSSTFVYNTVNTKIDQGAIDLHNVNTELTDLKARNSPDLDRVEDPADSASFFPDVWTL 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 181 RDFCLGLEIDQVLTPTDPEYLENSLRPKQSGDQVQNFNLPRLCIQKFPKKKCFIDPLPA 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 241 HOKKLAQLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLVTYN 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 241 HOKKLAQLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLVTYN 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 301 AISSGDLPCINAVLALAQRENSAAVQKAI AHYDQOMGQKQVQLPMTLOEILLDLHRTSER 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 361 EAI EVMKNSFKVDQSFQKELETLDDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVVLQKYLKSKSVSHAILQTDQAL 480
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 481 TETEKKKKEAQVKA EAKAEQAORLAAIQRONEQMMQERERLHQBQVROMETAKQNWLA EQ 540
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 541 QKMQEQQM 549
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 541 QKMQEQQM 549
```

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RESULT 9
US-10-137-865-46
; Sequence 46, Application US/10137865
; Publication No. US20030032155A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C154
; CURRENT APPLICATION NUMBER: US/10/137,865
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-865-46
Query Match 92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197; Indels 0; Gaps 0;
Matches 549; Conservative 0; Mismatches 0;
Oy 1 MALEIHMSDPMCLIFNFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLKNKLAG 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 61 KNGKFSVASTVQSHTKGIIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 61 KNGKFSVASTVQSHTKGIIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 121 LLSSTFVYNTVNTKIDQGAIDLHNVNTELTDLKARNSPDLDRVEDPADSASFFPDVWTL 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 181 RDFCLGLEIDQVLTPTDPEYLENSLRPKQSGDQVQNFNLPRLCIQKFPKKKCFIDPLPA 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 241 HOKKLAQLETLPPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLVTYN 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 301 AISSGDLPCINAVLALAQRENSAAVQKAI AHYDQOMGQKQVQLPMTLOEILLDLHRTSER 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 361 EAI EVMKNSFKVDQSFQKELETLDDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 421 KQGIYSKPGGHNLFQKTEELKAKYRPRKGIQAEVVLQKYLKSKSVSHAILQTDQAL 480
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 481 TETEKKKKEAQVKA EAKAEQAORLAAIQRONEQMMQERERLHQBQVROMETAKQNWLA EQ 540
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 541 QKMQEQQM 549
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 541 QKMQEQQM 549
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RESULT 10
US-10-140-474-46
; Sequence 46, Application US/10140474
; Publication No. US20030032156A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME
```

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; FILE REFERENCE: P3330RIC162
; CURRENT APPLICATION NUMBER: US/10/140,474
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-474-46

Query Match          92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEIHMSDPMCLINFNQKLVNQEALEILSAITQPVVVVAIVGLYRTGKSYLNKLAG 60
Db 1 MALEIHMSDPMCLINFNQKLVNQEALEILSAITQPVVVVAIVGLYRTGKSYLNKLAG 60
QY 61 KKGFSVASTVQSHTKGIWICVPHPNPNHTLVLLDTTEGLGDKADKNDIQIFALAL 120
Db 61 KKGFSVASTVQSHTKGIWICVPHPNPNHTLVLLDTTEGLGDKADKNDIQIFALAL 120
QY 121 LLSSTFVYNTVANKIDOGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDVLVWTL 180
Db 121 LLSSTFVYNTVANKIDOGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDVLVWTL 180
QY 181 RDFCLGLEIDGQLVTPDEYLENSLRPKQSGDQRVQNFNLPRLCIQKFFPKKCFIPDLPA 240
Db 181 RDFCLGLEIDGQLVTPDEYLENSLRPKQSGDQRVQNFNLPRLCIQKFFPKKCFIPDLPA 240
QY 241 HOKKLAQLETLDPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIWNGSRLKXNLVITYN 300
Db 241 HOKKLAQLETLDPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIWNGSRLKXNLVITYN 300
QY 301 ATSSGDLPCIEANVLALAQRENSAAVQKAIHYDQMGOKVOLPMETLQELLDLHRTSR 360
Db 301 ATSSGDLPCIEANVLALAQRENSAAVQKAIHYDQMGOKVOLPMETLQELLDLHRTSR 360
QY 361 EAIEVFMKNSFKVDQSFQKELETLLDAKQNDICKRNLEASDDYCSALLKDI FGPLEEAV 420
Db 361 EAIEVFMKNSFKVDQSFQKELETLLDAKQNDICKRNLEASDDYCSALLKDI FGPLEEAV 420
QY 421 KQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVILQKYLKSKESVSHAILQTDQAL 480
Db 421 KQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVILQKYLKSKESVSHAILQTDQAL 480
QY 481 TETEKKKKEAQVKAEEAKAEQAORLAAIQRNEQMQRERLHQBEOVRQMEIAKQNLAEQ 540
Db 481 TETEKKKKEAQVKAEEAKAEQAORLAAIQRNEQMQRERLHQBEOVRQMEIAKQNLAEQ 540
QY 541 QKMQEQQM 549
Db 541 QKMQEQQM 549

RESULT 11
US-10-142-431-46
; Sequence 46, Application US/10142431
; Publication No. US20030036179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC251
; CURRENT APPLICATION NUMBER: US/10/142,431
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-431-46

Query Match          92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEIHMSDPMCLINFNQKLVNQEALEILSAITQPVVVVAIVGLYRTGKSYLNKLAG 60
Db 1 MALEIHMSDPMCLINFNQKLVNQEALEILSAITQPVVVVAIVGLYRTGKSYLNKLAG 60
QY 61 KKGFSVASTVQSHTKGIWICVPHPNPNHTLVLLDTTEGLGDKADKNDIQIFALAL 120
Db 61 KKGFSVASTVQSHTKGIWICVPHPNPNHTLVLLDTTEGLGDKADKNDIQIFALAL 120
QY 121 LLSSTFVYNTVANKIDOGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDVLVWTL 180
Db 121 LLSSTFVYNTVANKIDOGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDVLVWTL 180
QY 181 RDFCLGLEIDGQLVTPDEYLENSLRPKQSGDQRVQNFNLPRLCIQKFFPKKCFIPDLPA 240
Db 181 RDFCLGLEIDGQLVTPDEYLENSLRPKQSGDQRVQNFNLPRLCIQKFFPKKCFIPDLPA 240
QY 241 HOKKLAQLETLDPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIWNGSRLKXNLVITYN 300
Db 241 HOKKLAQLETLDPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIWNGSRLKXNLVITYN 300
QY 301 ATSSGDLPCIEANVLALAQRENSAAVQKAIHYDQMGOKVOLPMETLQELLDLHRTSR 360
Db 301 ATSSGDLPCIEANVLALAQRENSAAVQKAIHYDQMGOKVOLPMETLQELLDLHRTSR 360
QY 361 EAIEVFMKNSFKVDQSFQKELETLLDAKQNDICKRNLEASDDYCSALLKDI FGPLEEAV 420
Db 361 EAIEVFMKNSFKVDQSFQKELETLLDAKQNDICKRNLEASDDYCSALLKDI FGPLEEAV 420
QY 421 KQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVILQKYLKSKESVSHAILQTDQAL 480
Db 421 KQGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVILQKYLKSKESVSHAILQTDQAL 480
QY 481 TETEKKKKEAQVKAEEAKAEQAORLAAIQRNEQMQRERLHQBEOVRQMEIAKQNLAEQ 540
Db 481 TETEKKKKEAQVKAEEAKAEQAORLAAIQRNEQMQRERLHQBEOVRQMEIAKQNLAEQ 540
QY 541 QKMQEQQM 549
Db 541 QKMQEQQM 549

RESULT 12
US-10-143-114-46
; Sequence 46, Application US/10143114
; Publication No. US20030036180A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
```

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; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C211
; CURRENT APPLICATION NUMBER: US/10/143,114
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-143-114-46

Query Match          92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEIHMSDPMCLIEFNQKLVNQEALEILSAITQPVVVAIVGLYRTGKSYLNMKLAG 60
DB 1 MALEIHMSDPMCLIEFNQKLVNQEALEILSAITQPVVVAIVGLYRTGKSYLNMKLAG 60

QY 61 KNGKFSVASTVQSHTKGIWICVPHNPWPNHTLVLLDTGEGLDVDEKADNKNDIQIFALAL 120
DB 61 KNGKFSVASTVQSHTKGIWICVPHNPWPNHTLVLLDTGEGLDVDEKADNKNDIQIFALAL 120

QY 121 LLSSTFVNTVNVKIDQGAIDLHNVTELTDLKARNSPDLDRVEDPADSASFPDLVWTL 180
DB 121 LLSSTFVNTVNVKIDQGAIDLHNVTELTDLKARNSPDLDRVEDPADSASFPDLVWTL 180

QY 181 RDFCLGLEIDQGLVTPDEYLENSLRPKQSGDQRVQNFNLPRLCIQKFFPKKCFIDPLA 240
DB 181 RDFCLGLEIDQGLVTPDEYLENSLRPKQSGDQRVQNFNLPRLCIQKFFPKKCFIDPLA 240

QY 241 HQKLAQLETLPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIWVNGSRLKNLVLYVN 300
DB 241 HQKLAQLETLPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIWVNGSRLKNLVLYVN 300

QY 301 AISSGDLPCIEENAVLALAQRENSAAVQKAI AHYDQMGQKQVQLPMETLQELLDLHRTSER 360
DB 301 AISSGDLPCIEENAVLALAQRENSAAVQKAI AHYDQMGQKQVQLPMETLQELLDLHRTSER 360

QY 361 EAI EVMKNSFKVDVQSFQKELETLLDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420
DB 361 EAI EVMKNSFKVDVQSFQKELETLLDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420

QY 421 KOGIYSPGGHNLFTQKTEELKAKYRPRKGIQAEV LQKYLKSKESVSHAILQTDQAL 480
DB 421 KOGIYSPGGHNLFTQKTEELKAKYRPRKGIQAEV LQKYLKSKESVSHAILQTDQAL 480

QY 481 TETEKKKKEAQQVKA EAKAEQAORLAAIORQNEQMMQERLHOEVROMETAKQNWLAEQ 540
DB 481 TETEKKKKEAQQVKA EAKAEQAORLAAIORQNEQMMQERLHOEVROMETAKQNWLAEQ 540

541 QKMQEQMQ 549
541 QKMQEQMQ 549

RESULT 13
US-10-142-419-46
; Sequence 46, Application US/10142419
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; Publication No. US2003004945A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C244
; CURRENT APPLICATION NUMBER: US/10/142,419
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-419-46

Query Match          92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEIHMSDPMCLIEFNQKLVNQEALEILSAITQPVVVAIVGLYRTGKSYLNMKLAG 60
DB 1 MALEIHMSDPMCLIEFNQKLVNQEALEILSAITQPVVVAIVGLYRTGKSYLNMKLAG 60

QY 61 KNGKFSVASTVQSHTKGIWICVPHNPWPNHTLVLLDTGEGLDVDEKADNKNDIQIFALAL 120
DB 61 KNGKFSVASTVQSHTKGIWICVPHNPWPNHTLVLLDTGEGLDVDEKADNKNDIQIFALAL 120

QY 121 LLSSTFVNTVNVKIDQGAIDLHNVTELTDLKARNSPDLDRVEDPADSASFPDLVWTL 180
DB 121 LLSSTFVNTVNVKIDQGAIDLHNVTELTDLKARNSPDLDRVEDPADSASFPDLVWTL 180

QY 181 RDFCLGLEIDQGLVTPDEYLENSLRPKQSGDQRVQNFNLPRLCIQKFFPKKCFIDPLA 240
DB 181 RDFCLGLEIDQGLVTPDEYLENSLRPKQSGDQRVQNFNLPRLCIQKFFPKKCFIDPLA 240

QY 241 HQKLAQLETLPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIWVNGSRLKNLVLYVN 300
DB 241 HQKLAQLETLPDDELEPEFVQVTEFCSYIFSHSMTKTLPGGIWVNGSRLKNLVLYVN 300

QY 301 AISSGDLPCIEENAVLALAQRENSAAVQKAI AHYDQMGQKQVQLPMETLQELLDLHRTSER 360
DB 301 AISSGDLPCIEENAVLALAQRENSAAVQKAI AHYDQMGQKQVQLPMETLQELLDLHRTSER 360

QY 361 EAI EVMKNSFKVDVQSFQKELETLLDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420
DB 361 EAI EVMKNSFKVDVQSFQKELETLLDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420

QY 421 KOGIYSPGGHNLFTQKTEELKAKYRPRKGIQAEV LQKYLKSKESVSHAILQTDQAL 480
DB 421 KOGIYSPGGHNLFTQKTEELKAKYRPRKGIQAEV LQKYLKSKESVSHAILQTDQAL 480

QY 481 TETEKKKKEAQQVKA EAKAEQAORLAAIORQNEQMMQERLHOEVROMETAKQNWLAEQ 540
DB 481 TETEKKKKEAQQVKA EAKAEQAORLAAIORQNEQMMQERLHOEVROMETAKQNWLAEQ 540

541 QKMQEQMQ 549
541 QKMQEQMQ 549
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Db      541 QKMQEQQM 549
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RESULT 14
US-10-123-262-46
; Sequence 46, Application US/10123262
; Publication No. US20030049816A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC38
; CURRENT APPLICATION NUMBER: US/10/123,262
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-262-46

Query Match      92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MALEIHMSDPMCLIEFNENQKVNQEALETLSAITOPVVVVAIVGLYRTGKSYLMNKL 60
Db      1 MALEIHMSDPMCLIEFNENQKVNQEALETLSAITOPVVVVAIVGLYRTGKSYLMNKL 60

QY      61 KNGGFSVASTVQSHYTKGIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
Db      61 KNGGFSVASTVQSHYTKGIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

QY      121 LLSSTFVYNTVANKIDQGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDDLVTWL 180
Db      121 LLSSTFVYNTVANKIDQGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDDLVTWL 180

QY      181 RDFCLGLEIDGQVLTPEDELEPEFVQVTFECSYIFSHSMTKTLPGGIMVNGSRLKNLVLYYV 240
Db      181 RDFCLGLEIDGQVLTPEDELEPEFVQVTFECSYIFSHSMTKTLPGGIMVNGSRLKNLVLYYV 240

QY      241 HOKKLAQLETLDPDELEPEFVQVTFECSYIFSHSMTKTLPGGIMVNGSRLKNLVLYYV 300
Db      241 HOKKLAQLETLDPDELEPEFVQVTFECSYIFSHSMTKTLPGGIMVNGSRLKNLVLYYV 300

QY      301 AISSGDLPCIENTAVLALAQRENSAAVQKAI AHYDQMGQKQVLPMTTLOELLDLHRTSER 360
Db      301 AISSGDLPCIENTAVLALAQRENSAAVQKAI AHYDQMGQKQVLPMTTLOELLDLHRTSER 360

QY      361 EALEVFMKNSFKDQVDSFOKELETLDAKQNDICKRNLEASSDYCSALLKDI FGPLEEAV 420
Db      361 EALEVFMKNSFKDQVDSFOKELETLDAKQNDICKRNLEASSDYCSALLKDI FGPLEEAV 420

QY      421 KQGIYKPGGHNLFIQKTEELKAKYRPRKGIQAEVVLQKYLKSKSVSHAILQTDQAL 480
Db      421 KQGIYKPGGHNLFIQKTEELKAKYRPRKGIQAEVVLQKYLKSKSVSHAILQTDQAL 480

Db      541 QKMQEQQM 549
|||||
TETETKKKEAAQVKAEEAKAEQAORLAAIQORNEQMMQERERLHOEVRQWIEAKQNLWLAQ 540
|||||
TETETKKKEAAQVKAEEAKAEQAORLAAIQORNEQMMQERERLHOEVRQWIEAKQNLWLAQ 540
|||||
QKMQEQQM 549
|||||
QKMQEQQM 549
|||||
RESULT 15
US-10-142-423-46
; Sequence 46, Application US/10142423
; Publication No. US20030049817A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC249
; CURRENT APPLICATION NUMBER: US/10/142,423
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 46
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-423-46

Query Match      92.5%; Score 2815; DB 14; Length 586;
Best Local Similarity 100.0%; Pred. No. 8.2e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MALEIHMSDPMCLIEFNENQKVNQEALETLSAITOPVVVVAIVGLYRTGKSYLMNKL 60
Db      1 MALEIHMSDPMCLIEFNENQKVNQEALETLSAITOPVVVVAIVGLYRTGKSYLMNKL 60

QY      61 KNGGFSVASTVQSHYTKGIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
Db      61 KNGGFSVASTVQSHYTKGIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALAL 120

QY      121 LLSSTFVYNTVANKIDQGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDDLVTWL 180
Db      121 LLSSTFVYNTVANKIDQGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDDLVTWL 180

QY      181 RDFCLGLEIDGQVLTPEDELEPEFVQVTFECSYIFSHSMTKTLPGGIMVNGSRLKNLVLYYV 240
Db      181 RDFCLGLEIDGQVLTPEDELEPEFVQVTFECSYIFSHSMTKTLPGGIMVNGSRLKNLVLYYV 240

QY      241 HOKKLAQLETLDPDELEPEFVQVTFECSYIFSHSMTKTLPGGIMVNGSRLKNLVLYYV 300
Db      241 HOKKLAQLETLDPDELEPEFVQVTFECSYIFSHSMTKTLPGGIMVNGSRLKNLVLYYV 300

QY      301 AISSGDLPCIENTAVLALAQRENSAAVQKAI AHYDQMGQKQVLPMTTLOELLDLHRTSER 360
Db      301 AISSGDLPCIENTAVLALAQRENSAAVQKAI AHYDQMGQKQVLPMTTLOELLDLHRTSER 360

QY      421 KQGIYKPGGHNLFIQKTEELKAKYRPRKGIQAEVVLQKYLKSKSVSHAILQTDQAL 480
Db      421 KQGIYKPGGHNLFIQKTEELKAKYRPRKGIQAEVVLQKYLKSKSVSHAILQTDQAL 480
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Qy	361	EAIEVFMKNSFKVDVDSFOKELETLLDAKONDICKRNLEASSDYCSALLKDI FGPLEEAV	420
Db	361	EAIEVFMKNSFKVDVDSFOKELETLLDAKONDICKRNLEASSDYCSALLKDI FGPLEEAV	420
Qy	421	KGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVLOKYLKSKSVSHAILQTDQAL	480
Db	421	KGIYSKPGGHNLFIOKTEELKAKYRPRKGIQAEVLOKYLKSKSVSHAILQTDQAL	480
Qy	481	TETEKKKKEAQVKAEEAKAEQRLAAIQRNEQMMQERERLHQEQVRQMEIAKQNWLAEQ	540
Db	481	TETEKKKKEAQVKAEEAKAEQRLAAIQRNEQMMQERERLHQEQVRQMEIAKQNWLAEQ	540
Qy	541	QKMQEQQMQ	549
Db	541	QKMQEQQMQ	549

Search completed: May 20, 2005, 13:44:05
 Job time : 138 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 20, 2005, 13:09:27 ; Search time 42 Seconds
(without alignments)
1353.907 Million cell updates/sec

Title: US-10-659-549-3
Perfect score: 3043
Sequence: 1 MALEIHMSDPKCLIENTNEQ.....GEARSCSQGVMSQKVVW 591

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1958.5	64.4	592	2 A41268	guanine nucleotide
2	1897	62.3	591	2 S70524	guanine nucleotide
3	1765.5	58.0	589	2 A46459	macrophage-activat
4	1757.5	57.8	591	2 S43506	hypothetical prote
5	1365.5	44.9	623	2 I49684	guanylate binding
6	251.5	8.3	555	2 T17320	hypothetical prote
7	216	7.1	217	2 A84810	probable guanylate
8	213.5	7.0	991	2 H86188	hypothetical prote
9	171.5	5.6	4574	2 G02520	plectin - human
10	171.5	5.6	4684	2 A59404	plectin (imported)
11	160.5	5.3	1291	2 T23382	hypothetical prote
12	160.5	5.3	1690	2 T13030	microtubule bindin
13	160.5	5.3	4687	1 A39638	plectin - rat
14	159.5	5.2	862	2 T49593	hypothetical prote
15	158	5.2	464	2 H90279	microtubule bindin
16	156.5	5.1	1410	1 A57013	early endosome ant
17	155.5	5.1	762	2 T50155	hypothetical prote
18	154.5	5.1	853	2 T23697	hypothetical prote
19	154.5	5.1	1392	2 A43356	microtubule-vesicl
20	154.5	5.1	1427	2 S22695	restin - human
21	153	5.0	944	2 S26710	spindle pole body
22	151.5	5.0	992	2 T46337	hypothetical prote
23	151	5.0	1290	2 A55094	chromosomal protei
24	151	5.0	1818	1 S73852	hypothetical prote
25	148	4.9	577	1 S39804	moesin - pig
26	148	4.9	1288	2 T46486	chromosomal protei
27	147.5	4.8	429	2 S29565	apolipoprotein A-I
28	147.5	4.8	1790	2 S67593	transport protein
29	147	4.8	407	2 S23325	M2 protein precurs

30	146	4.8	586	1 B41129	ezrin - mouse
31	146	4.8	742	2 S56337	hypothetical prote
32	146	4.8	925	2 T01384	hypothetical prote
33	145.5	4.8	1426	2 T00337	hypothetical prote
34	145	4.8	742	2 C91265	probable vimentin
35	145	4.8	742	2 H86105	probable vimentin
36	144	4.8	1178	2 S78475	mannosylphosphoryl
37	144	4.7	871	2 D86355	protein T16E15.12
38	144	4.7	980	2 E71606	hypothetical prote
39	143.5	4.7	864	2 B90395	purine NTPase [imp
40	143.5	4.7	1875	2 S38173	myosin-like protei
41	143.5	4.7	1992	2 A47297	myosin heavy chain
42	142.5	4.7	1164	2 T24806	hypothetical prote
43	142.5	4.7	2442	2 T08621	centrosome associa
44	142	4.7	657	2 S05517	lamin - chicken
45	142	4.7	1972	1 A41604	myosin heavy chain

ALIGNMENTS

RESULT 1

A41268
guanine nucleotide-binding protein 1 - human
C:Species: Homo sapiens (man)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: A41268
R:Cheng, Y.S.E.; Patterson, C.E.; Staeheli, P.
Mol. Cell. Biol. 11, 4717-4725, 1991
A>Title: Interferon-induced guanylate-binding proteins lack an N(T)KXD consensus motif a
A:Reference number: A41268; MUID:91342675; PMID:1715024
A:Accession: A41268
A:Molecule type: mRNA
A:Residues: 1-592 <CHE>
A:Cross-references: UNIPROT:P32455; GB:M55542; NID:g183001; PIDN:AAA35871.1; PID:g183002
C:Genetics:
A:Gene: GDB:GBP1
A:Cross-references: GDB:378351; OMIM:600411
A:Map position: lpter-lqter
C:Superfamily: guanine nucleotide-binding protein 1

Query Match 64.4%; Score 1958.5; DB 2; Length 592;
Best Local Similarity 69.4%; Pred. No. 7.6e-101;
Matches 387; Conservative 71; Mismatches 89; Indels 11; Gaps 3;

Qy	1	MALEIHMSDPKCLIENTNEQKVNQEALETLSAITOPVVVVAIVGLYRTGKSYLMNKL	60
Db	1	MASEIHMTGPMCLIENTNGRLMANPEALKILSAITQPMVVVAIVGLYRTGKSYLMNKL	60
Qy	61	KNKGFSVASTVQSHTKGIWCVPHNPNHLLVLLDTEGLGDVEKADNKNDIQIFALAL	120
Db	61	KNKGFSIGSVQSHTKGIWCVPHNPNHLLVLLDTEGLGDVEKADNKNDIQIFALAV	120
Qy	121	LLSSTFVYNTVNVKIDQAGAILDLHNVTETLLKARNSPD--LDRVDPADSSAPFPDL	178
Db	121	LLSSTFVYNSIGTINQAMQQLYVVTETLTHIRSKSPDENENEVEDSADFVSFPDFV	180
Qy	179	TLRDFCLGLEIDGQLVTPDEYLENSLRPKQSDORVQNFNPLRLCIQKFFPKKCF	238
Db	181	TLRDFSLDLEADGQPLTFDEYLYTLKLGKGTOKDETFLRLCIRKFFPKKCFV	240
Qy	239	PAHQKLAQLTLPDDLEPEFVQVTEFCSYIFSHSMTKTLPGIYVNGSRKLNVLTY	298
Db	241	PVHRKLAQLKLEQDELDPEFVQVADFCSYIFSNKTKLTSGLIYVNGSRKLNVLTY	300
Qy	299	VNAISSGDLPCFENAVIALAQRENSAAVQKAIHYDQMGQKQVLPMTLQELDLH	358
Db	301	VNAISSGDLPCFENAVIALAQRENSAAVQKAIHYEQMGQKQVLPMTLQELDLH	360
Qy	359	EREAIEVFMKNSFKVDQSQFQKELETLLDKQNDICRNLEASSDYCSALLKDI	418
Db	361	EREAIEVFIKNSFKVDQSQFQKELETLLDKQNDICRNLEASSDYCSALLKDI	420

QY 301 AISSGDLPCINAVLALAQRENSAAVOKAIAHYDOOMQGVOLPMTLOELLDLHRTSER 360
DB 301 AICSGELPCMENAVLTLLAQIENSAVOKAITYEEQNNQKTHMPTETLOELLDLHRTSER 360
QY 361 EAIEVFMKNSFKVDVQSFQKELETLLDAKONDICKRNLEASSDYCSALLKIDIFGLPEAV 420
DB 361 EAIEVFMKNSFKVDVQSFQKELEGAQLEAKRAFAVKKNDMSAHCSDDLLEGLFAHLEEV 420
QY 421 KOGIYSKPGGHNLFQKTEELKAKYYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
DB 421 KOGTFYKPGGYVFLQKQLEKKYIQTPKGLQAEVLMRLKYFESKEDLADTLLKMDQSL 480
QY 481 TETEKKEAQAQKAEAEQAORLAAIQORNEQMMQERERLHOEVRO-----METAKQNW 536
DB 481 TEKEKQIEWEIRIKAEAAANRALAEAMQKQHEMLMEQEQSYQEHMKQLTETKMEQERKEL 540
QY 537 LAEQO-----KMQEQO 547
DB 541 MAEQRIISLKLOQE 556

RESULT 4
S43506
hypothetical protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S43506
R:Asundi, V.K.; Stahl, R.C.; Showalter, L.; Conner, K.J.; Carey, D.J.
Biochim. Biophys. Acta 1217, 257-265, 1994
A:Title: Molecular cloning and characterization of an isoprenylated 67 kDa protein.
A:Reference number: S43506; MUID:94198287; PMID:8148370
A:Accession: S43506
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-591 <ASU>
A:Cross-references: UNIPROT:Q63563; EMBL:N80367; NID:G207604; PIDN:AAA19909.1; PID:G2076
C:Superfamily: guanine nucleotide-binding protein 1

Query Match 57.8%; Score 1757.5; DB 2; Length 591;
Best Local Similarity 63.3%; Pred. No. 9.5e-90;
Matches 346; Conservative 82; Mismatches 116; Indels 3; Gaps 1;

QY 1 MALEIHMSDPCLIENFNEQKVNQAELEILSAITOPVVVVAIVGLYRTGKSYLMNKLAKGFSVAS 60
DB 3 NASEBIHMQMCLIENTEAHLVINQAEALRIILSAINQPPVVVVAIVGLYRTGKSYLMNKLAKG 62
QY 61 KNGKPSVASTVQSHTKGIMWCVPHPNPNHTLLDTEGLGDVEKADNKNNDIQIFALAL 120
DB 63 KRTGSLGSTVQSHTKGIMWCVPHPKAGQTLVLLDTEGLEDEKVGNDQNDQIFALAV 122
QY 121 LLSSTFVYNTVTKIDQGAIDLHNVTELTLLKARNSPDLDRVEDPADSASFFPDLVMTL 180
DB 123 LLSSTFVYNSGTINQOAMDQLHYVTELTLLKSSPDSQSDGIDDSANFVCFPTFWAL 182
QY 181 RDPCLGLEIDQLVTPDEYLENSLRPKGSDQVQNFNLPRLCTIQKFPFKKCFIFDLPA 240
DB 183 RDFSLELVNGKLVTPDEYLSHSLTLKKGADKTKSFNEPRLCIRKFPFKKCFIFDRPA 242
QY 241 HOKLAQLETLDPDELEPEFVQVTEPCSYIFSHMTKTLPGGIWNGSRLLKNLVLTYN 300
DB 243 LRKQCKLTGEBELCEFEVQAEFTSYIFSYSAVTKLSGGIIVNGPRLKSLVQTVYG 302
QY 301 AISSGDLPCINAVLALAQRENSAAVOKAIAHYDOOMQGVOLPMTLOELLDLHRTSER 360
DB 303 AISSGSLPCMESAVLTLLAQIENSAVOKAITYEEQNNQKTHMPTETLOELLDLHRLIER 362
QY 361 EAIEVFMKNSFKVDVQSFQKELETLLDAKONDICKRNLEASSDYCSALLKIDIFGLPEAV 420
DB 363 EAIEIFLNKNSPKVDVQSFQKELETLLGKRAFIKNSDVSSAHCSDDLIEDIFGLPEEV 422
QY 421 KOGIYSKPGGHNLFQKTEELKAKYYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
DB 423 KOGTFYKPGGYVFLQKQLEKKYINQAPKGLAEAVLKKYFESKEDIVETLLKTDQSL 482

QY 481 TETEKKEAQAQKAEAEQAORLAAIQORNEQMMQERERLHOEVROMEIAKQNWLAEQ 540
DB 483 TEAAKEITEVERIKAEATAEAAANRELAEKQKFEMLMQKEESYQEHVROL---TEKMKSEQ 539
QY 541 QKMQEQO 547
DB 540 KKLIEEQ 546

RESULT 5
I49684
guanylate binding protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49684
R:Wynn, T.A.; Nicolet, C.M.; Paulnock, D.M.
J. Immunol. 147, 4384-4392, 1991
A:Title: Identification and characterization of a new gene family induced during macroph
A:Reference number: A46459; MUID:92091752; PMID:1753106
A:Accession: I49684
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-623 <RES>
A:Cross-references: UNIPROT:Q61594; GB:M81128; NID:gl93443; PIDN:AAA37668.1; PID:gl93444
C:Superfamily: guanine nucleotide-binding protein 1

Query Match 44.9%; Score 1365.5; DB 2; Length 623;
Best Local Similarity 49.3%; Pred. No. 4.5e-68;
Matches 267; Conservative 112; Mismatches 150; Indels 13; Gaps 3;

QY 10 PMCLIEFNEQKVNQAELEILSAITOPVVVVAIVGLYRTGKSYLMNKLAKGKGFVSAS 69
DB 8 PICLVENHNEQLSVNQAIEILDKISQPPVVVVAIVGWSHTGKSYLMNCLAGNHVFPPLGS 67
QY 70 TVQSHHTGIMWCVPHPNPNHTLLDTEGLGDVEKADNKNNDIQIFALALLSSTFTYV 129
DB 68 TVQSQTGIMWCVPHPHTKPEHTLLVLLDTEGLGDVEKADPKNDLWIFALSLLSSTFTYV 127
QY 130 TVNKIDQGAIDLHNVTELTLLKARNSPDLDRVEDPADSASFFPDLVMTLRDQCLGLEI 189
DB 128 SMNTINQAELEQLHYVTELTLLIRAKSPNPHGINKSTEFVSFPDFVMTVRDFMLELKL 187
QY 190 DGQLVTPDEYLENSLRPKGSDQVQNFNLPRLCTIQKFPFKKCFIFDLPAHQKL-AQL 248
DB 188 NGEDITSDEVLENALKLIPGNPPIQASNSARECIRFFPNRKCFVFEWPTHDIELIKQL 247
QY 249 ETLPPDELEPEFVQVTEPCSYIFSHMTKTLPGGIWNGSRLLKNLVLTYNALSSGDL 308
DB 248 ETISEDQLDPTFKESAMAFASYIFTYAKIKTLREGIKVTGNGGLTGLTVTVYVDAINS 307
QY 309 CIENAVLALAQRENSAAVOKAIAHYDOOMQGVOLPMTLOELLDLHRTSREAEVPMK 368
DB 308 CLDDAVTTLAQRENSAAVOKAASHYSEQAQRSLPTDITIOELLDVHAACKEAMAVPME 367
QY 369 NSFQKVDQSFQKELETLLDAKONDICKRNLEASSDYCSALLKIDIFGLPEEAVKQGIYK 428
DB 368 HSFQDENQQLFKLVLELLREKNGFLFKNEEASDKYQCEELDRLSKOLMDNI--STFSVP 425
QY 429 GGHNLFTQKTEELKAKYYRPRKGIQAEVLQKYLKSKESVSHAILQTDQALTEKTKK 488
DB 426 GGHRLYMDREKIEHDYQVPRKGVKASEVFQNFQSQAIIESSILQADTALTAGAKAIA 485
QY 489 EAQVKAQAEAEQAORLAAIQORNEQMMQERERLHOEVROMEIAKQNWLAEQKQWQEQ 548
DB 486 EKHTKEAEAEKQDQLLRQKEHQEYMEAEQKRNKENLEQ-----RRKLEQERE 535
QY 549 QV 550
DB 536 QL 537

RESULT 6

Qy	479	ALTETEKKE-----AQVKAERAEAKORLAAIORQNEQMMOERERLHQ	523
Db	217	ELIEAQKKHDERITKLEESTKLEQAVQELIEAQKKHDERITYKLE-ESIQKLVDAQRRAE	275
Qy	524	EQVRQMEIAKQNWLABEQQKMQEQMVFNCFISPL-PVTMRVCSS--OKEG---EAARS	577
Db	276	ERIAKLENAVEQ-LVEAQKRTDER-----ITKLEEVTKLVESQLGMQNEIRELRKA	326
Qy	578	CGSQQGVWSQ	587
Db	327	LGSMDKRWGR	336

Search completed: May 20, 2005, 13:28:53
Job time : 46 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 20, 2005, 13:21:01 ; Search time 179 Seconds
(without alignments)
1690.720 Million cell updates/sec

Title: US-10-659-549-3
Perfect score: 3043
Sequence: 1 MALEIHMSDPMLLIENFNEQ.....GEAARSCGQGVWSQKVVV 591

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2815	92.5	586	1 GBP5_HUMAN	Q96pp8 homo sapien
2	2516	82.7	489	2 Q86TMS	Q86tm5 homo sapien
3	2490	81.8	504	2 Q8NF03	Q8nf03 homo sapien
4	2236	73.5	481	2 Q8N4Q4	Q8n4q4 homo sapien
5	1958.5	64.4	592	1 GBP1_HUMAN	P32455 homo sapien
6	1933	63.5	724	2 Q8BMN7	Q8bm7 mus musculus
7	1907.5	62.7	590	1 GBP5_MOUSE	Q8cfb4 mus musculus
8	1905.5	62.6	561	2 Q8BU78	Q8bu78 mus musculus
9	1897	62.3	591	1 GBP2_HUMAN	P32456 homo sapien
10	1892	62.2	591	2 Q8PH05	Q8ph05 homo sapien
11	1774.5	58.3	563	2 Q8H0R5	Q8h0r5 homo sapien
12	1765.5	58.0	589	1 GBP1_MOUSE	Q81514 mus musculus
13	1764	58.0	481	2 Q8TCE5	Q8tce5 homo sapien
14	1757.5	57.8	589	1 GBP2_RAT	Q63663 rattus norv
15	1750.5	57.5	589	1 GBP2_MOUSE	Q920e6 mus musculus
16	1528.5	50.2	638	2 Q8N8V2	Q8n8v2 homo sapien
17	1510.5	49.6	633	2 Q8ZN66	Q8zn66 homo sapien
18	1500.5	49.3	640	1 GBP4_HUMAN	Q96pp9 homo sapien
19	1498.5	49.2	640	2 Q8NSL0	Q8nsl0 homo sapien
20	1493.5	49.1	633	2 Q7Z3F0	Q7z3f0 homo sapien
21	1482.5	48.7	638	2 Q8BU48	Q8bu48 mus musculus
22	1482.5	48.7	641	2 Q8KAN1	Q8kan1 mus musculus
23	1479.5	48.6	632	2 Q81Z40	Q81z40 mus musculus
24	1468.5	48.3	620	2 Q8VECS	Q8vec5 mus musculus
25	1459.5	48.0	620	2 Q81107	Q81107 mus musculus
26	1407	46.2	612	2 Q8CFA8	Q8cfa8 mus musculus
27	1392.5	45.8	611	2 Q8ZQL8	Q8zql8 mus musculus
28	1389.5	45.6	611	2 Q8NV33	Q8nv33 homo sapien
29	1377.5	45.3	611	2 Q8PEN2	Q8pen2 mus musculus
30	1365.5	44.9	623	2 Q61594	Q61594 mus musculus
31	1344	44.2	619	2 Q6PG83	Q6pg83 mus musculus

RESULT 1

ID	GBPS_HUMAN	STANDARD	PRT	586 AA
AC	Q96PP8			
DT	29-MAR-2004	(Rel. 43, Created)		
DT	05-JUL-2004	(Rel. 44, Last annotation update)		
DE	Interferon-induced guanylate-binding protein 5 (GTP-binding protein 5)			
DE	(Guanine nucleotide-binding protein 5) (GBP-TA antigen)			
DE	(UNQ2427/PRO4987)			
GN	Name=GBP5;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_taxid=9606;			
RN	[1]_taxid=9606;			
RN	SEQUENCE FROM N.A.			
RA	Avdalovic A., Fu H., Tsurushita N.;			
RT	"Human GBP-4 and -5: new members of the IFN-gamma-inducible guanylate-binding protein family.";			
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Eichmueller S., Hartmann T., Thiel D., Usener D., Dummer R.,			
RA	Schadendorf D.;			
RT	"GBP-TA: a new tumor-specific antigen of cutaneous lymphoma depicted by serological detection.";			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yanaura D.,			
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,			
RA	Godowski P., Gray A.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";			
RL	Genome Res. 13:2265-2270(2003).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins P.S., Wagner K.H., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			

Q6gn80 xenopus lae
Q8bts3 mus musculus
Q6dcs7 xenopus lae
Q7t0s6 xenopus lae
Q66j21 xenopus lae
Q66ir9 xenopus lae
Q6yl1 oncorhynch
Q6dhp7 brachydanio
Q8k0g1 mus musculus
Q6p3v3 homo sapien
Q90892 gallus gall
Q6pc12 xenopus lae
Q7cmv8 mus musculus
Q66k09 mus musculus

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- SIMILARITY: Belongs to the GBP family.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF288815; AAL02055.1; -;
DR EMBL; AF430642; AAN39035.1; -;
DR EMBL; AF430643; AAN39036.1; -;
DR EMBL; AY358953; AAO89312.1; -;
DR EMBL; BC031639; AAH31639.1; -;
DR HSSP; P32455; 1DG3.
DR Genew; HGNC:19895; GBP5.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; GBP; 1.
DR Pfam; PF02841; GBP; 1.
KW GTP-binding; Lipoprotein; Multigene family; Prenylation.
FT NP_BIND 45 52 GTP (By similarity).
FT NP_BIND 97 101 GTP (By similarity).
FT LIPID 583 583 S-geranylgeranyl cysteine (By
similarity).
SQ SEQUENCE 586 AA; 66617 MW; 95DDC02F0FB705D0 CRC64;
Query Match 92.5%; Score 2815; DB 1; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.7e-134;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALEIHMSDPMCLIEFNQKLVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
DB 1 MALEIHMSDPMCLIEFNQKLVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
QY 61 KNGFSAVSTVQSHTKGIWICVPHNPWNHNTLVLLDTGLGDKVEKADNKNNDIIFALAL 120
DB 61 KNGFSAVSTVQSHTKGIWICVPHNPWNHNTLVLLDTGLGDKVEKADNKNNDIIFALAL 120
QY 121 LLSSTFYNTVTKIDQGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDLVWTL 180
DB 121 LLSSTFYNTVTKIDQGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDLVWTL 180
QY 181 RDFCLGLEIDGQVLTDPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCFIFDLPA 240
DB 181 RDFCLGLEIDGQVLTDPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCFIFDLPA 240
QY 241 HQKLAQLETPDDELEPEFVQVTFCSYIFSHSMTKTLPGGIWNGSRKLNVLVTYN 300
DB 241 HQKLAQLETPDDELEPEFVQVTFCSYIFSHSMTKTLPGGIWNGSRKLNVLVTYN 300
QY 301 AISSGDLPCLENVLAQRENSAAVQKAIAHYDQMGQKQVQLPMETQLDHLHTSER 360
DB 301 AISSGDLPCLENVLAQRENSAAVQKAIAHYDQMGQKQVQLPMETQLDHLHTSER 360
QY 361 EAIEVFMKNSFKVDQSGFQKELETLLDAKQNDICKRNLEASSYCSALLKDIFGPLEEAV 420
DB 361 EAIEVFMKNSFKVDQSGFQKELETLLDAKQNDICKRNLEASSYCSALLKDIFGPLEEAV 420

QY 421 KOGIYSPGHNLFIOKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
DB 421 KOGIYSPGHNLFIOKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
QY 481 TETEKKEAQAQKAEAEKAEQAQRLAAIQORNEQWQERERLHQBQVQWETAKQNWLAEQ 540
DB 481 TETEKKEAQAQKAEAEKAEQAQRLAAIQORNEQWQERERLHQBQVQWETAKQNWLAEQ 540
QY 541 QKMQEQQMQ 549
DB 541 QKMQEQQMQ 549
RESULT 2
Q86TWS PRELIMINARY; PRT; 489 AA.
ID Q86TWS
AC Q86TWS; (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE CTCL tumor antigen GBP-5ta (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cutaneous lymphoma;
RX PubMed=14996095;
RA Hartmann T.B., Thiel D., Dummer R., Schadendorf D., Eichmuller S.;
RT "SEREX identification of new tumour-associated antigens in cutaneous
T-cell lymphoma.";
RL Br. J. Dermatol. 150:252-258 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cutaneous lymphoma;
RX PubMed=15175044;
RA Fellenberg F., Hartmann T.B., Dummer R., Usener D., Schadendorf D.,
RA Eichmuller S.;
RT "GBP-5 splicing variants: New guanylate-binding proteins with tumor-
associated expression and antigenicity.";
RL J. Invest. Dermatol. 122:1510-1517 (2004).
DR EMBL; AF328727; AAO40731.1; -;
DR HSSP; P32455; 1DG3.
DR GO; GO:0005525; F-GTP binding; IEA.
DR GO; GO:0003924; F-GTPase activity; IEA.
DR GO; GO:0006955; P-immune response; IEA.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; GBP; 1.
DR Pfam; PF02841; GBP; 1.
DR NON_TER 489_489
FT SEQUENCE 489 AA; 55247 MW; B493C3586DFFDA1D CRC64;
Query Match 82.7%; Score 2516; DB 2; Length 489;
Best Local Similarity 99.8%; Pred. No. 1.8e-119;
Matches 488; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALEIHMSDPMCLIEFNQKLVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
DB 1 MALEIHMSDPMCLIEFNQKLVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
QY 61 KNGFSAVSTVQSHTKGIWICVPHNPWNHNTLVLLDTGLGDKVEKADNKNNDIIFALAL 120
DB 61 KNGFSAVSTVQSHTKGIWICVPHNPWNHNTLVLLDTGLGDKVEKADNKNNDIIFALAL 120
QY 121 LLSSTFYNTVTKIDQGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDLVWTL 180
DB 121 LLSSTFYNTVTKIDQGAIDLLHNVTETDLLKARNSPDLDRVEDPADSASFPDLVWTL 180
QY 181 RDFCLGLEIDGQVLTDPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCFIFDLPA 240
DB 181 RDFCLGLEIDGQVLTDPDEYLENSLRPKQSDQVQNFNLPRLCIQKFFPKKCFIFDLPA 240

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Qy 241 HOKKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLVTYN 300
Db 241 HOKKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLVTYN 300
Qy 301 AISSGDLPCIEENAVLALAQRENSAAVQKAI AHYDOQMGQKQVQLPMTLQELLDLHRTSER 360
Db 301 AISSGDLPCIEENAVLALAQRENSAAVQKAI AHYDOQMGQKQVQLPMTLQELLDLHRTSER 360
Qy 361 EAI EFMKNSFKVDQSFQKLETLDDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420
Db 361 EAI EFMKNSFKVDQSFQKLETLDDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420
Qy 421 KOGIYSPGGHNLFIQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
Db 421 KOGIYSPGGHNLFIQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
Qy 481 TETKKKKE 489
Db 481 TETKKKKE 489
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RESULT 3

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Q8NF03 Q8NF03 PRELIMINARY; PRT; 504 AA.
AC Q8NF03;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE FLJ00401 protein (Fragment).
GN Name=FLJ00401;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090479; BAC03460.1; -.
DR HSSP; P32455; 1DG3.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0006955; P:Immune response; IEA.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; GBP_1.
DR Pfam; PF02841; GBP_C; 1.
FT NON_TER 1
FT NON_TER 504
SQ SEQUENCE 504 AA; 56862 MW; 37E814E34539F743 CRC64;
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Query Match 81.8%; Score 2490; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 3.9e-118; Indels 0; Gaps 0;
Matches 483; Conservative 0; Mismatches 0;

Qy 1 MALEIHSMDPNCMLIENFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 60
Db 22 MALEIHSMDPNCMLIENFNEQLKVNQEALEILSAITQPVVVAIVGLYRTGKSYLMNKLKAG 81
Qy 61 KNGFSVASTVQSHTKGIWICVPHNPWNHTLVLLDTEGLGDVEKADKNNDIQIFALAL 120
Db 82 KNGFSVASTVQSHTKGIWICVPHNPWNHTLVLLDTEGLGDVEKADKNNDIQIFALAL 141
Qy 121 LLSSTFVYNTVTKIDQGAIDLLHNVTETDILLKARNSPDLDRVEDPADSASFFPDVWTL 180
Db 142 LLSSTFVYNTVTKIDQGAIDLLHNVTETDILLKARNSPDLDRVEDPADSASFFPDVWTL 201
Qy 181 RDFCLGLEIDQLVTPDEYLENSLRPKQSGDQRVQNFNLPRLCIQKFPKKCFIFDLPA 240
Db 202 RDFCLGLEIDQLVTPDEYLENSLRPKQSGDQRVQNFNLPRLCIQKFPKKCFIFDLPA 261
Qy 241 HOKKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLVTYN 300
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Db 262 HOKKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLVTYN 321
Qy 301 AISSGDLPCIEENAVLALAQRENSAAVQKAI AHYDOQMGQKQVQLPMTLQELLDLHRTSER 360
Db 322 AISSGDLPCIEENAVLALAQRENSAAVQKAI AHYDOQMGQKQVQLPMTLQELLDLHRTSER 381
Qy 361 EAI EFMKNSFKVDQSFQKLETLDDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 420
Db 382 EAI EFMKNSFKVDQSFQKLETLDDAKNDICRNL EASSDYCSALLKDI FGPLEEAV 441
Qy 421 KOGIYSPGGHNLFIQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
Db 442 KOGIYSPGGHNLFIQKTEELKAKYRPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 501
Qy 481 TET 483
Db 502 TET 504
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RESULT 4

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Q8N4Q4 Q8N4Q4 PRELIMINARY; PRT; 481 AA.
AC Q8N4Q4;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Similar to guanylate binding protein 5 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033761; AAH33761.1; -.
DR HSSP; P32455; 1DG3.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0006955; P:Immune response; IEA.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; GBP_1.
DR Pfam; PF02841; GBP_C; 1.
FT NON_TER 1
FT NON_TER 481
SQ SEQUENCE 481 AA; 55070 MW; 3E642C58BCA06895 CRC64;
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Query Match 73.5%; Score 2236; DB 2; Length 481;
Best Local Similarity 99.8%; Pred. No. 2.6e-105;
Matches 439; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 110 KNDIQIFALALLISSTFVYNTVTKIDQGAIDLLHNVTETDILLKARNSPDLDRVEDPADS 169
Db 5 KNDIQIFALALLISSTFVYNTVTKIDQGAIDLLHNVTETDILLKARNSPDLDRVEDPADS 64
Qy 170 ASFPFDLVWTLRDFCLGLEIDQLVTPDEYLENSLRPKQSGDQRVQNFNLPRLCIQKFP 229
Db 65 ASFPFDLVWTLRDFCLGLEIDQLVTPDEYLENSLRPKQSGDQRVQNFNLPRLCIQKFP 124
Qy 230 KKKCFIFDLPAHQKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGS 289
Db 125 KKKCFIFDLPAHQKLAQLETLPPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIMVNGS 184
Qy 290 RLKLNVLTYNATSSGDLPCIEENAVLALAQRENSAAVQKAI AHYDOQMGQKQVQLPMTLQ 349
Db 185 RLKLNVLTYNATSSGDLPCIEENAVLALAQRENSAAVQKAI AHYDOQMGQKQVQLPMTLQ 244
Qy 350 ELLDLHRTSREAEIEVFMKNSFKVDQSFQKLETLDDAKNDICRNL EASSDYCSALL 409
Db 245 ELLDLHRTSREAEIEVFMKNSFKVDQSFQKLETLDDAKNDICRNL EASSDYCSALL 304
Qy 410 KDIFGPLEEAVKQGIYSPGGHNLFIQKTEELKAKYRPRKGIQAEVLQKYLKSKESV 469
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Db 305 KDIFGPLEEAVKQGIYKPGKHNLFIQKTEELKAKYRPRKGIQAEVQLKYLKSKESV 364
Qy 470 SHAIILOTDALTEKTEKKKEAQVKAFAEKAQRLAAIQRONEQWQERLHQBQVROM 529
Db 365 SHAIILOTDALTEKTEKKKEAQVKAFAEKAQRLAAIQRONEQWQERLHQBQVROM 424
Qy 530 EIAKQNLWAEQQKMQBQQMQ 549
Db 425 EIAKQNLWAEQQKMQBQQMQ 444

RESULT 5
GBP1_HUMAN
ID GBP1_HUMAN STANDARD; PRT; 592 AA.
AC F32455;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interferon-induced guanylate-binding protein 1 (GTP-binding protein 1)
DE (Guanine nucleotide-binding protein 1) (hUGBP-1).
GN Names=GBP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=91342675; PubMed=1715024;
RA Cheng Y.-S.E., Patterson C.E., Staeheli P.;
RT "Interferon-induced guanylate-binding proteins lack an N(terminal)KXD
RT consensus motif and bind GMP in addition to GDP and GTP.";
RL Mol. Cell. Biol. 11:4717-4725(1991).
RN [2]
SEQUENCE FROM N.A.
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueclin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gichman J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
ISOPRENOL.
RX MEDLINE=96427476; PubMed=8830800;
RA Nantais D.E., Schwenmle M., Stickney J.T., Vestal D.J., Buss J.E.;
RT "Prenylation of an interferon-gamma-induced GTP-binding protein: the
RT human guanylate binding protein, huGBP1.";
RL J. Leukoc. Biol. 60:423-431(1996).
RN [5]
X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX
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RX MEDLINE=20140138; PubMed=10676968; DOI=10.1038/35000617;
RA Prakash B., Praecke K.J.K., Renault L., Wittinghofer A., Herrmann C.;
RT "Structure of human guanylate-binding protein 1 representing a unique
RT class of GTP-binding proteins.";
RL Nature 403:567-571(2000).
CC -!- FUNCTION: Binds GTP, GDP and GMP.
CC -!- INDUCTION: By interferon gamma during macrophage activation.
CC -!- SIMILARITY: Belongs to the GBP family.
CC
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CC
CC EMBL; M55542; AAA35871.1; -.
CC EMBL; BT006847; AAP35493.1; -.
CC EMBL; BC002666; AAH02666.1; -.
CC EIR; A41268; A41268.
CC PDB; 1DG3; X-ray; A=1-592.
CC PDB; 1FSN; X-ray; A=1-592.
CC Genew; HGNC:4182; GBP1.
CC H-InvDB; HIX0018119; -.
CC MIM; 600411; -.
CC CO; GO:0005525; F:GTP binding; TAS.
CC InterPro; IPR003191; GBP.
CC Pfam; PF02263; GBP; 1.
CC Pfam; PF02841; GBP C; 1.
KW 3D-structure; GTP-Binding; Interferon induction; Lipoprotein;
KW Multigene family; Polymorphism; Prenylation.
FT NP_BIND 45 52 GTP.
FT NP_BIND 97 101 GTP.
FT LIPID 589 589 S-farnesyl cysteine.
FT VARIANT 349 349 S -> T (in dbSNP:1048425).
FT
FT STRAND 11 17
FT TURN 18 19
FT STRAND 20 23
FT HELIX 25 32
FT TURN 33 33
FT STRAND 37 46
FT TURN 47 48
FT HELIX 51 58
FT TURN 59 60
FT STRAND 78 84
FT TURN 89 90
FT STRAND 92 98
FT STRAND 101 101
FT HELIX 104 106
FT TURN 110 111
FT HELIX 112 122
FT STRAND 125 131
FT HELIX 136 140
FT TURN 141 142
FT HELIX 143 146
FT TURN 147 147
FT HELIX 148 151
FT STRAND 153 153
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FT HELIX 171 174
FT STRAND 177 183
FT TURN 184 184
FT HELIX 198 205
FT TURN 206 206
FT HELIX 214 229
FT STRAND 233 237
FT HELIX 244 252
FT HELIX 255 257
FT HELIX 260 276
FT STRAND 281 282
FT TURN 283 285
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DR GO: 0006955; P: immune response; IEA.
DR InterPro: IPR003191; GBP.
DR Pfam: PF02263; GBP; 1.
DR Pfam: PF02841; GBP; C; 1.
SQ SEQUENCE 724 AA; 799C517B51DBF47C CRC64;

Query Match 63.5%; Score 1933; DB 2; Length 724;
Best Local Similarity 64.9%; Pred. No. 8.e-90;
Matches 392; Conservative 70; Mismatches 126; Indels 16; Gaps 5;

QY 1 MALEIHMSPMCLIEFNQKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
DB 1 MAPEIHMPEPLCLIGSTEGHVLNQEAALKILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
QY 61 KNGKFSVASTVQSHTKGIWICVPHNPNHTLVLDTEGLGDNVEKADNKNDIQIFALAL 120
DB 61 KEKGFSGVSTVQSHTKGIWICVPHNPNHTLVLDTEGLGDNVEKADNKNDIQIFALAI 120
QY 121 LLSSTFVYNTVTKIDQAGIDLLHNVTETDLKARNSPDLDRV--EDPADSASFFPDVLV 178
DB 121 LLSSTFVYNTVTKIDQAGIDLLHNVTETDLKARNSPDLDRV--EDPADSASFFPDVLV 178
QY 179 TLRDFCLGLIEDQVTPDEYLENSLRPKQSGDQVRQNFNLRCLCIQKFFPKKCFIFDL 238
DB 180 TLRDFCLGLIEDQVTPDEYLENSLRPKQSGDQVRQNFNLRCLCIQKFFPKKCFIFDL 238
QY 239 PAHQKLAQLTLPDDELPFVQVTEPCSYIFSHSMYKTLPGGIWNGSRKLNVLTY 298
DB 240 PALGSKLSQLPTLSNELNSDFVQDLSEFCSHFTQSKTTLPGGIQVNGPRLESVLTY 299
QY 299 VNAISSGDLPCIEENAVLAAQRENSAOKAIAHYDQOGKQVQLPMETLQELLDLHRTS 358
DB 300 VDAINSGLPSTVNTVTLARRENSAOKAIAHYDQOGKQVQLPMETLQELLDLHRTC 359
QY 359 EREAIEFVKNSPKVDQSFQKELETLDLQAKNDICRNLLEASDYCSALLKIDIFGLPEE 418
DB 360 EREAIEFVKNSPKVDQSFQKELETLDLQAKNDICRNLLEASDYCSALLKIDIFGLPEE 418
QY 419 AVKQGIYSPGHNLIQKTEELKAKYRPRKIQAEVQLKYLKSKESVSHALITDQ 478
DB 420 EVAQEFYHKGKGLFLQREQLKANYRQPGKGTQAEVQLYLYNAKETVSTVITLQTDQ 479
QY 479 ALTETKKEKAEQVKAQAEKAEQALAAIQORQEQMMQRERLHQSVQRMETAKQWLA 538
DB 480 VLTDKIQSKAEQAEKAEKAEQALAAIQORQEQMMQRERLHQSVQRMETAKQWLA 539
QY 539 EQQMQEQQQQ---VFINCPIFSL-----PVTMRVCSGKGEKAARSQSGQGWQ 587
DB 540 EQQWILKQRAQRCPIWCLDLLAEDGPKQDLSQKLCFCGQEG--GRLSGAEDGAASE 597
QY 588 KVVW 591
DB 598 ALWI 601

RESULT 7
GBP5_MOUSE STANDARD; PRT; 590 AA.
ID GBP5_MOUSE
AC Q8CFB4; Q8CFB4;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon-induced guanylate-binding protein 5 (GTP-binding protein 5)
DE (Guanine nucleotide-binding protein 5) (MuGBP-5).
GN Names=Gbpb5;
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster;
RC MEDLINE=22284156; PubMed=12396730; DOI=10.1089/107999002760274926;
RX
```

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RA Nguyen T.T., Hu Y., Widney D.P., Mar R.C., Smith J.B.;
RT "Murine GBP-5, a new member of the murine guanylate-binding protein
RT family, is coordinately regulated with other GBPs in vivo and in
RT vitro.";
RL J. Interferon Cytokine Res. 22:899-909 (2002).
RN [2]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RA Adams M., Mural R.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RP STRAIN=NMRI; TISSUE=Breast tumor;
RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- SIMILARITY: Belongs to the GBP family.
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CC -----
CC EMBL; AF422243; AAN31451.1; -
CC EMBL; AY128412; AAN46362.1; -
CC EMBL; BC058555; AAH58555.1; -
CC HSSP; P32455; 1DG3.
CC MGD; MGI:2429943; Gbp5.
CC InterPro: IPR003191; GBP.
CC Pfam; PF02263; GBP; 1.
CC Pfam; PF02841; GBP; C; 1.
KW GTP-binding; Lipoprotein; Multigene family; Prenylation.
FT NP BIND 45 52 GTP (By similarity).
FT NP BIND 97 101 GTP (By similarity).
FT LIPID 587 587 S-gexanylgeryl cysteine (By
FT similarity).
FT KXA -> T (in Ref. 2).
FT CONFLICT 488 490 K -> E (in Ref. 2).
FT CONFLICT 501 501
SQ SEQUENCE 590 AA; 66970 MW; 092C0B3F3E0E2D26 CRC64;

Query Match 62.7%; Score 1907.5; DB 1; Length 590;
Best Local Similarity 68.5%; Pred. No. 1.3e-88;
Matches 379; Conservative 62; Mismatches 103; Indels 9; Gaps 3;

QY 1 MALEIHMSPMCLIEFNQKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
DB 1 MAPEIHMPEPLCLIGSTEGHVLNQEAALKILSAITQPVVVVAIVGLYRTGKSYLMNKLKAG 60
QY 61 KNGKFSVASTVQSHTKGIWICVPHNPNHTLVLDTEGLGDNVEKADNKNDIQIFALAL 120
DB 61 KEKGFSGVSTVQSHTKGIWICVPHNPNHTLVLDTEGLGDNVEKADNKNDIQIFALAI 120
QY 121 LLSSTFVYNTVTKIDQAGIDLLHNVTETDLKARNSPDLDRV--EDPADSASFFPDVLV 178
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Db 121 LLSSTFFVNTMKNIDQGAIDLHNVTELTDLTRNSDSNQTEGEGPAD-MSFFPDLVW 179
Qy 179 TLRDFCLGLEIDGQAVTPDDEYLENSLRPKQSDQVQNFNLPRLCIQFFPKKCFIDL 238
Db 180 TLRDFFLDQANGHAITSDEYLENSLKLKQSDERTQTFNLPRLCIQFFPKKCFVDA 239
Qy 239 PAHQKLAQLETLDPDELEPFVQVTFPCSYIFSHSMTKTLPGGIMVNGSRLKNLVITY 298
Db 240 PALGSKLSQLEPLTSLNEELNSDFVODLSEFCSHIFTQSKTKTLPGGIVNGPRLSLVLY 299
Qy 299 VNATSSGDLPCENAVLALAQRENSAAVQKAIAHYDQOMQKVOLPMETLOELDLHRTS 358
Db 300 VDAINSGLPSEIENVTVTLARRENSAAVQKAIGHYDQMSKVQTFETLOELDLHRTC 359
Qy 359 EREAIEFWKNSFDVDSFOKELETLDDAKQNDICKNLEASSDYCSALLKIDIFGPLEE 418
Db 360 EREAIEFRKHSFDGEFFQKELESLSAKQDEICKKNADASAALCSTLGSIFKPQLEQ 419
Qy 419 AVKQIYKPGGHNLFIOKTELBKAKYRPRKGIQAEBVLQKYLKSKESVSHAILQTDQ 478
Db 420 EVAQEFYKPGGKHLFLQRMQQLKANYRQPKGTQABEVLQTYLNAKETVSRITLQTDQ 479
Qy 479 ALTETEKKKKAQVKAERAKAQAOLAIQONEQMQERELHQEVQVOMEIAK----- 533
Db 480 VLTDKEIQKKAQERAEARLKAQRLAIRIQEQRKAEMERQHQEQRLQIALEKARVAQ 539
Qy 534 -QNWLAEQKQMOE 545
Db 540 EQWILKQRAQEE 552

RESULT 8
Q8BU78 PRELIMINARY; PRT; 561 AA.
ID Q8BU78
AC Q8BU78
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched
DE library, clone:E030025M22 product:weakly similar to GUANYLATE BINDING
DE PROTEIN 5 (Fragment).
GN Name=Gbp5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBT_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6875(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA The FANTOM Consortium,
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RL "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multiplexed sequencer.";
RL Genome Res. 10:1757-1771 (2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuura T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK087083; BAC39801.1;
DR HSSP; P32455; IDG3.
DR MGD; MGI:2429943; Gbp5.
DR GO; GO:0005252; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; GBP_1.
DR Pfam; PF02841; GBP_C; 1.
DR NON TER 561
FT SEQUENCE 561 AA; 63322 MW; 2C83B9838661FF39 CRC64;
SQ
Query Match 62.6%; Score 1905.5; DB 2; Length 561;
Best Local Similarity 69.0%; Pred. No. 1.6e-88;
Matches 380; Conservative 60; Mismatches 108; Indels 3; Gaps 2;
Qy 1 MALEIHSMDPCLTLENFNEQLKVNQEALEILSALTQPVVVAIVGLYRTGKSYLMNKLKAG 60
Db 1 MAPEIHPPEPLCLIGSTEGHLVTNQEALEILSALTQPVVVAIVGLYRTGKSYLMNKLKAG 60
Qy 61 KNKGFSVASTVQSHTKGIWICVPHNPNTLVLDTGLGDEVEKADNNDIQIFALAL 120
Db 61 KEKGFSVGSVQSHTKGIWICVPHNPNTLVLDTGLGDEVEKADNNDIQIFALAI 120
Qy 121 LLSSTFFVNTMKNIDQGAIDLHNVTELTDLKARNSPDLDRV--EDPADSASFPDLVW 178
Db 121 LLSSTFFVNTMKNIDQGAIDLHNVTELTDLTRNSDSNQTEGEGPAD-MSFFPDLVW 179
Qy 179 TLRDFFCLGLEIDGQAVTPDDEYLENSLRPKQSDQVQNFNLPRLCIQFFPKKCFIDL 238
Db 180 TLRDFFLDQANGHAITSDEYLENSLKLKQSDERTQTFNLPRLCIQFFPKKCFVDA 239
Qy 239 PAHQKLAQLETLDPDELEPFVQVTFPCSYIFSHSMTKTLPGGIMVNGSRLKNLVITY 298
Db 240 PALGSKLSQLEPLTSLNEELNSDFVODLSEFCSHIFTQSKTKTLPGGIVNGPRLSLVLY 299
Qy 299 VNATSSGDLPCENAVLALAQRENSAAVQKAIAHYDQOMQKVOLPMETLOELDLHRTS 358
Db 300 VDAINSGLPSEIENVTVTLARRENSAAVQKAIGHYDQMSKVQTFETLOELDLHRTC 359
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QY 359 EREAIEVFMKNSGKVDQSFQKELETLLDAKQNDICRNLLEASDYCSALLKDIQFGLPEE 418
Db 360 EREAIEIFRKHSPKDSGEFFQKELESLSAKQDEICKKNADASAALCSTLLGSIPKPLEQ 419
QY 419 AVKQGISYSPGGHNLFIQKTEELKAKYREPRKGIQAEVLQKYLKSKESVSHAILQTDQ 478
Db 420 EVAQEFYHYPGGHKLFLQMEQLKANYRQPGKGTQAEVLQTLNNAKETVSRITLIQTDQ 479
QY 479 ALTETEKKKKEAQVKAEEAKAEAAQRLAAIQRONEQMMQERERLHOVQVOMEIAQNWLA 538
Db 480 VLTDKEIQKABQERAEARLEAQRLEAIRIOEQRKAEMERQHQQLRQIALEKARVAQ 539
QY 539 EQQKMOEQMQ 549
Db 540 EQQWILKQRAQ 550

RESULT 9
GBP2_HUMAN
ID _GBP2_HUMAN STANDARD; PRT; 591 AA.
AC P32456; Q86TB0.
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon-induced guanylate-binding protein 2 (GTP-binding protein 2)
DE (Guanine nucleotide-binding protein 2) (HuGBP-2).
GN Names=GBP2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=91342675; PubMed=1715024;
RA Cheng Y.-S.E., Patterson C.E., Staeheli P.;
RT "Interferon-induced guanylate-binding proteins lack an N(7)KXD
RT consensus motif and bind GMP in addition to GDP and GTP.";
RL Mol. Cell. Biol. 11:4717-4725(1991).
RN [2]
RN REVISIONS.
RC TISSUE=Forebrain;
RA Schwemmler M.;
RL Submitted (SEP-1991) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Pouscka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.-W., Weil B., Amid C., Fobo G., Han M., Osanger A.,
RA Wiemann S.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Binds GTP, GDP and GMP.
CC -!- INDUCTION: By interferon gamma during macrophage activation.
CC -!- SIMILARITY: Belongs to the GBP family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M55543; AAA67323.1; -.
CC EMBL; AL832451; CAD89925.1; -.
CC DR PIR; S70524; S70524.
CC DR HSSP; P32455; 1DG3.
CC DR Genew; HGNC:4183; GBP2.
CC DR H-InvDB; HIX0000764; -.
CC DR MIM; 600412; -.
CC DR GO; GO:0005525; F:GTP binding; TAS.
CC DR GO; GO:0006955; P:Immune response; TAS.
CC DR InterPro; IPR003191; GBP.
CC DR Pfam; PF02263; GBP; 1.
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DR Pfam; PF02841; GBP_C; 1.
KW GTP-binding; Interferon induction; Lipoprotein; Multigene family;
KW Prenylation.
FT NP_BIND 45 52 GTP (By similarity).
FT NP_BIND 97 101 GTP (By similarity).
FT LIPID 588 588 S-geranylgeranyl cysteine (By
FT similarity).
FT CONFLICT 303 303 S -> G (in Ref. 3).
SQ SEQUENCE 591 AA; 67183 MW; E090809EE18FC8A8 CRC64;

Query Match 62.3%; Score 1897; DB 1; Length 591;
Best Local Similarity 63.5%; Pred. No. 4.6e-88;
Matches 377; Conservative 88; Mismatches 101; Indels 28; Gaps 4;

QY 1 MALEIHMSDPMCLIEFNENBOLKVNQBALEILSAITQPVVVVAIVGLYRTGKSYLMNKLGA 60
Db 1 MAPEINLPQPMSLIDNTKGQLVNFEALKLSAITQPVVVVAIVGLYRTGKSYLMNKLGA 60
QY 61 KNGGFSVASTVQSHTKGIWICVPHNPWNHPTLVLLDTTEGLGDVEKADNKNDIQIFALAL 120
Db 61 KXGFGSLGSTVKSHTKGIWMCVPHPKPEHTLVLLDTTEGLGDIEKGDNENDSWIFALAI 120
QY 121 LLSSTFVNTVNTKIDQGAIDLHNTVELTDLKARNSPDLDRVEDPADSASFPPDLVWTL 180
Db 121 LLSSTFVNSMGTIINQAMDQLHYVTELTDRIKANSSPGNNNSVDDPSADFVSFPFVWTL 180
QY 181 RPFCLGLEIDGOLVTPDEVLENLRPKQSGDQDVQNFNLPRLCIOKFFPKKCFIDLPA 240
Db 181 RDTLELEVDGEPITADDYELSLSLRKGTDKKSKSFNDPRLCIRKFFPKKCFVDFWPA 240
QY 241 HOKKLAQLETLDPDELEPEFVQQTVEFCSYIFSHSMTKTPGGIMVNGSRLKNLVTYVN 300
Db 241 PKKYLAHLQLEKEELNPDFIEQVAEFCSYILSHSNVKTLSGGIAVNGPRLSLSLVTYVN 300
QY 301 A1SSGDLPCIEANAVIALAQRNSAAVQKAIHYDQMGQKQVLPMTLEQLDLHRTSR 360
Db 301 A1SSGDLPCMENAVIALAQIENSAVQKAIHYEQMGQKQVLPMTLEQLDLHRTSR 360
QY 361 EAIEVFMKNSPKVDQSFQKELETLLDAKQNDICRNLLEASDYCSALLKDIQFGLPEEAV 420
Db 361 EAIEVFMKNSFKVDQMFQKLEAQRDDFCQNSKASSDCCWALLQDIFGPLEEDV 420
QY 421 KQGIYSKPGGHNLFIQKTEELKAKYREPRKGIQAEVLQKYLKSKESVSHAILQTDQAL 480
Db 421 KQGTFSKPGGYRLFTQKLQELKNKYQVPRKGIQAEVLKYLKYLESKEDVADALLQTDQSL 480
QY 481 TTEKKKKEAQVKAEEAKAEAAQRLAAIQRONEQMMQERERLHOVQVQVRO----WEIAQNW 536
Db 481 SEKEKAIEVERIKAESEAAAKQMLEBIQKNEEMMEQEKESYQEHVKQLTEKMERDRAQL 540
QY 537 LAEQQ-----KMOEQMQVFINCFISPLPVTWVCSGSGEAGAAASCGSQQGVW 585
Db 541 MAEQKTLALQLEQE-----RLKKGFEENSKR---LQKDIW 575

RESULT 10
Q6GPH0
ID Q6GPH0 PRELIMINARY; PRT; 591 AA.
AC Q6GPH0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Guanylate binding protein 2, interferon-inducible.
GN Name=GBP2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA Klausner R.D., Collins E.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bozak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073163; AAH73163.1; -.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; GBP; 1.
DR Pfam; PF02841; GBP; 1.
SQ SEQUENCE 591 AA; 67233 MW; 739CE562AF335776 CRC64;
Query Match 62.2%; Score 1892; DB 2; Length 591;
Best Local Similarity 63.5%; Pred. No. 8.2e-88;
Matches 377; Conservative 87; Mismatches 102; Indels 28; Gaps 4;
Qy 1 MALEIHMSDPCLNENFNEQKVNQAELEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
Db 1 MAPEINLPGLMSLDNTRKQGLVWNPPEALKILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
Qy 61 KNGGFSVASTVQSHTKGIWICVPHNPNTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
Db 61 KNGGFSLGSTVKSHTKGIWICVPHNPNTLVLLDTEGLGDVEKADNKNDISWIFALAI 120
Qy 121 LLSSTFVYNTVNTKIDQGAIDLHNVNLTDLKARNSPDLDRVEDPADSASFFPDVWTL 180
Db 121 LLSSTFVYNSGNTINQAMDQVHYVTELTDRIKANSSFGNNSVDDSDAFVFFFAFWTL 180
Qy 181 RDCFLGLEIDQVTPDEYENSLRPKQSDQVQNFNLPRLCIQKFPFKKCFIFDLPA 240
Db 181 RDTLELEVDGEPIADDDYLSLKLKRGTKDKSKSFNDPRLCIRKFPFKKCFVFDWPA 240
Qy 241 HQKLAQLETLDPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIWNGSRKLNVLVTYN 300
Db 241 PKKYLAHLEQKBEELNPDTEQVAEFCSYIFLSHNVKTLGGIPVNGPRLESVLVTYN 300
Qy 301 AISSGDLPCIEAVNALAQRNSAAVQKAIHYDQMGQKQVQLPMETLQELLDLHRTSER 360
Db 301 AISSGDLPCRENAVVALAQIENSAVAEKAIHYEQMGQKQVQLPTELTQELLDLHRTSER 360
Qy 361 EAIEVFMKNSFKVDQSQFQKELETLLDAKQNDICRNLKLEASSDYCSALLKIDIFGLEAV 420
Db 361 EAIEVFMKNSFKVDQSQFQKELETLLDAKQNDICRNLKLEASSDYCSALLKIDIFGLEAV 420
Qy 421 KQGIYSKPGGHNLFIOKTEELKAKYPRKGIQAEVQLKYSKESVSHAIQTQDAL 480
Db 421 KQGTFSKPGGYRLFTQKLELNKYYQVPRKGIQAEVQLKYSKESVSHAIQTQDAL 480
Qy 481 TETEKKEKAEQVAKAEKAEQVAKAEQVAKAEQVAKAEQVAKAEQVAKAEQVAKAEQVAK 536
Db 481 SEKEKAEVERIKAEAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAE 540

Qy 537 LAEQ-----KMQEQMQVFNCFISPLPVTNRVCSGKEGEAARSCSQGQVW 585
Db 541 MAEQETKLLALKEQE-----RLKKEGFENESKR-----LQKDIW 575

RESULT 11
Q9H0R5 PRELIMINARY; PRT; 563 AA.
AC Q9H0R5;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hypothetical protein DKFZp564C2478.
GN Name=DKFZp564C2478;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RG The German cDNA Consortium;
RA Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaiipp A.,
RA Mewes H.W., Weil B., Amlid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL136680; CAB66615.1; -.
DR HSSP; P32455; 1DG3.
DR Genew; HGNC:4184; GBP3.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR003191; GBP.
DR Pfam; PF02263; GBP; 1.
DR Pfam; PF02841; GBP; 1.
KW Hypothetical protein.
SQ SEQUENCE 563 AA; 64127 MW; 0C2FB7CE7FFCBCC3 CRC64;

Query Match 58.3%; Score 1774.5; DB 2; Length 563;
Best Local Similarity 65.4%; Pred. No. 6.8e-82;
Matches 363; Conservative 61; Mismatches 90; Indels 41; Gaps 3;
Qy 1 MALEIHMSDPCLNENFNEQKVNQAELEILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
Db 1 MAPEIHMTGPMCLINTENGELVANPEALKILSAITQPVVVAIVGLYRTGKSYLNKLAG 60
Qy 61 KNGGFSVASTVQSHTKGIWICVPHNPNTLVLLDTEGLGDVEKADNKNDIQIFALAL 120
Db 61 KNGGFSLGSTVKSHTKGIWICVPHNPNTLVLLDTEGLGDVEKADNKNDISWIFTLAV 120
Qy 121 LLSSTFVYNTVNTKIDQGAIDLHNVNLTDLKARNSPDLDRVEDPADSASFFPDVWTL 180
Db 121 LLSSTLVYNSGNTINQAMDQVHYVTELTDRIRKSSPDENEDSADFVFFPDVWTL 180
Qy 181 RDCFLGLEIDQVTPDEYENSLRPKQSDQVQNFNLPRLCIQKFPFKKCFIFDLPA 240
Db 181 RDFSLEADQQLTPDEYLEYSLKLTQGN----- 210
Qy 241 HQKLAQLETLDPDELEPEFVQVTEFCSYIFSHSMTKTLPGGIWNGSRKLNVLVTYN 300
Db 211 --RKLQLEKLEQDELDPEFVQVADFCYSIFSNSTKTLGGIKVNGPCLESVLVTYN 268
Qy 301 AISSGDLPCIEAVNALAQRNSAAVQKAIHYDQMGQKQVQLPMETLQELLDLHRTSER 360
Db 269 AISRGDLPCRENAVVALAQIENSAVAEKAIHYDQMGQKQVQLPTELTQELLDLHRTSER 328
Qy 361 EAIEVFMKNSFKVDQSQFQKELETLLDAKQNDICRNLKLEASSDYCSALLKIDIFGLEAV 420
Db 329 EAIEVFMKNSFKVDHFLQKLAQLEKADKRDGFCQKQAEASSDRCSALLQVIFSPLEBEV 388
Qy 421 KQGIYSKPGGHNLFIOKTEELKAKYPRKGIQAEVQLKYSKESVSHAIQTQDAL 480
Db 389 KAGIYSKPGGYCLFIQKLEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKEKKEK 448

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2].
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC022272; AAH22272.1; -;
 DR HSSP: P32455; 1DC3.
 DR GO: GO:0005525; F:GTP binding; IEA.
 DR GO: GO:0003924; F:GTPase activity; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR003191; GBP.
 DR Pfam: PF02263; GBP; 1.
 DR Pfam: PF02841; GBP; C; 1.
 SQ SEQUENCE 481 AA; 54034 MW; 2F8B6G6EA92EED87 CRC64;

 Query Match 58.0%; Score 1764; DB 2; Length 481;
 Best Local Similarity 71.1%; Pred. No. 1.9e-81;
 Matches 342; Conservative 64; Mismatches 75; Indels 0; Gaps 0;

 QY 1 MALEIHMSDPMCLINFEQKLVNQEALEILSAITQPVVVAIVGLYRTGSKYLMNKLKAG 60
 DB 1 MAPEINLPQMSLIDNTKQGLVWNEALKILSAITQPVVVAIVGLYRTGSKYLMNKLKAG 60

 QY 61 KNGFSVASTVQSHTKGIWICVPHNPVHTLVLLDTGEGLDVEKADKNNDIQIFALAL 120
 DB 61 KNGFSLGSTVKSHTKGIWMCVPHPKKPEHTLVLLDTGEGLDIEKGNENDSWIFALAI 120

 QY 121 LLSSTFVYNTVNTKIDQGAIDLLHNVTETLTLKARNSPDLRVEDPADSASFFPDVWTL 180
 DB 121 LLSSTFVYNSMGITNQAMDQLHYVTELTDLKARNSPGNNSVDDSDAFVFFAFVWTL 180

 QY 181 RDFCLGLEIDQVTPDEYLENSLRPKQSGDQVRQNFNLPRLCIOKFPKKKCFIFDLPA 240
 DB 181 RDFTELEVDGEPIITADDYLESLKLRKGTDKSKSFNDPRLCIRKFPKPKCFVFWPA 240

 QY 241 HQKLAOLETLPDDELEPEFVQVTEPCSYIFSHMTKTLPGGIMVNGSRKLVLTYYN 300
 DB 241 PKTYLAHLEQKEELNPDFIEQVAEFCSTYLSHNVKTLTSGGIPVNGPRLESILVLTYYN 300

 QY 301 AISSGDLPCIEANVLAQRENSAAVOKAIAHYDQMGOKVQLPMTLOELDLHRTSER 360
 DB 301 AISSGDLPCMENAVLAQIENSAAVEAIAHYDQMGOKVQLPMTLOELDLHRTSER 360

 QY 361 EAIEVFMKSNFKVDQSQFQKELETLLDAKNDICRNLEASSDYCSALLKDIQFGLPEAV 420
 DB 361 EAIEVFMKSNFKVDQSQFQKELETLLDAKNDICRNLEASSDYCSALLKDIQFGLPEAV 420

 QY 421 KQGYSKPGGHNLFQKTEELKAKYRPRKGIQAEEVLQKYLKSKESVSHAILQDQAL 480
 DB 421 KQGYTSKPGGVRLLFTQKLELKNKYQVPRKGIQAEEVLKYLESKEDVADALLQDQSL 480

 QY 481 T 481
 DB 481 S 481

 RESULT 14
 ID GBP2_RAT
 AC Q63663;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interferon-induced guanylate-binding protein 2 (GTP-binding protein 2)
 DE (Guanine nucleotide-binding protein 2) (p67).
 GN Name=Gbp2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1].
 RP SEQUENCE FROM N.A.; TISSUE SPECIFICITY, AND ISOPRENOID
 RX MEDLINE=94198287; PubMed=8148370; DOI=10.1016/0167-4781(94)90284-4;
 RA Asundi V.K., Stahl R.C., Showalter L., Conner K.J., Carey D.J.;
 RT "Molecular cloning and characterization of an isoprenylated 67 kDa
 protein.";
 RL Biochim. Biophys. Acta 1217:257-265(1994).
 CC -!- FUNCTION: Binds GTP, GDP and GMP (By similarity).
 CC -!- TISSUE SPECIFICITY: Ubiquitous.
 CC -!- INDUCTION: By interferon gamma.
 CC -!- SIMILARITY: Belongs to the GBP family.
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M80367; AAA19909.1; ALT_INIT.
 CC PIR: S43506; S43506.
 DR HSSP: P32455; 1DC3.
 DR InterPro: IPR003191; GBP.
 DR Pfam: PF02263; GBP; 1.
 DR Pfam: PF02841; GBP; C; 1.
 KW GTP-binding; Interferon induction; Lipoprotein; Multigene family;
 KW Prenylation.
 FT NP_BIND 45 52 GTP (By similarity).
 FT NP_BIND 97 101 GTP (By similarity).
 FT LIPID 586 S-geranylgeranyl cysteine.
 SQ SEQUENCE 589 AA; 67109 MW; 5E52B79102CD97F CRC64;

 Query Match 57.8%; Score 1757.5; DB 1; Length 589;
 Best Local Similarity 63.3%; Pred. No. 5.2e-81;
 Matches 346; Conservative 82; Mismatches 116; Indels 3; Gaps 1;

 QY 1 MALBIHMSDPMCLINFEQKLVNQEALEILSAITQPVVVAIVGLYRTGSKYLMNKLKAG 60
 DB 1 MASBIHMLQPMCLIENTEAHLVINQEALEILSAINQPVVVVAIVGLYRTGSKYLMNKLKAG 60

 QY 61 KNGFSVASTVQSHTKGIWICVPHNPVHTLVLLDTGEGLDVEKADKNNDIQIFALAL 120
 DB 61 KRTGFSLGSTVQSHTKGIWMCVPHPKKAGQTLVLLDTGEGLDVEKGNQNDWIFALAV 120

 QY 121 LLSSTFVYNTVNTKIDQGAIDLLHNVTETLTLKARNSPDLRVEDPADSASFFPDVWTL 180
 DB 121 LLSSTFVYNSMGITNQAMDQLHYVTELTDLKARNSPDQSGIDDSANFVGFPTFWAL 180

 QY 181 RDFCLGLEIDQVTPDEYLENSLRPKQSGDQVRQNFNLPRLCIOKFPKKKCFIFDLPA 240
 DB 181 RDFSLELVNGKLVTPDEYLEHSLTLTKGADKKTSPNEPRLCIRKFPKPKCFIFDRPA 240

 QY 241 HQKLAOLETLPDDELEPEFVQVTEPCSYIFSHMTKTLPGGIMVNGSRKLVLTYYN 300
 DB 241 LRKQLCKLETGEEELCEFEVQVAEFTSYIFSYSAVKTVGGIIVNGPRLSLVLTYYN 300

 QY 301 AISSGDLPCIEANVLAQRENSAAVOKAIAHYDQMGOKVQLPMTLOELDLHRTSER 360
 DB 301 AISSGSLPCMESAVTLAQIENSAAVOKAIAHYEQMNQKIOMPTETLOELDLHRLIER 360

 QY 361 EAIEVFMKSNFKVDQSQFQKELETLLDAKNDICRNLEASSDYCSALLKDIQFGLPEAV 420
 DB 361 EAIBIFLKNQFKVDQKQFQTELGNLILSKRDAFIKKNSDVSSAHCSLDIEDIFGLPEBEV 420

QY 421 KGIYSKPGGHNLFQIKTBTLLKAKYVREPRKGIQAEVLQKYLKSKSVSHAILQDQAL 480
 Db KQITSPKGGYFLQMRQELKKYNQAPKGLAEAVLKQYFESKEDIVETLLKTDQSL 480
 QY 481 TETKXKKAQVKAQAEKAEQALAAIQRONQWQERLHQEVRQWEIAKQWLABQ 540
 Db TEARKEIEVIRIKAEATAEARELAKEQBKFELMQQKEESYOEHVRLQ---TEKWKERQ 537
 QY 541 QKMQEQQ 547
 Db 538 KKLIEQ 544

RESULT 15
 GBP2_MOUSE
 ID GBP2_MOUSE STANDARD; PRT; 589 AA.
 AC Q9Z056; Q8CIC6; Q921N2; Q9RI10;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interferon-induced guanylate-binding protein 2 (GTP-binding protein 2)
 DE (Guanine nucleotide-binding protein 2) (mGBP2) (mGBP-2).
 GN Name=GBP2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=99077537; PubMed=9862701;
 RA Boehm U., Gueethlein L., Klamp T., Ozbek K., Schaub A., Fuetterer A.,
 RA Pfeiffer K., Howard J.C.;
 RT "Two families of GTPases dominate the complex cellular response to
 RT IFN-gamma";
 RL J. Immunol. 161:6715-6723(1998).
 RN [2]
 RP SEQUENCE FROM N.A., and ISOPRENOL.
 RC STRAIN=C57BL/6; TISSUE=Bone marrow;
 RX MEDLINE=99074031; PubMed=9858320;
 RA Vestal D.J., Buss J.E., McKercher S.R., Jenkins N.A., Copeland N.G.,
 RA Kelnier G.S., Asundi V.K., Maki R.A.;
 RT "Murine GBP-2: a new IFN-gamma-induced member of the GBP family of
 RT GTPases isolated from macrophages";
 RL J. Interferon Cytokine Res. 18:977-985(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Kidney;
 RX MEDLINE=99313432; PubMed=10386861; DOI=10.1089/107999099313938;
 RA Anderson S.L., Carton J.M., Zhang X., Rubin B.Y.;
 RT "Genomic organization and chromosomal localization of a new member of
 RT the murine interferon-induced guanylate-binding protein family";
 RL J. Interferon Cytokine Res. 19:487-494(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalilus D.E.,

RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Binds GTP, GDP and GMP (By similarity).
 CC -!- INDUCTION: By interferon gamma during macrophage activation.
 CC -!- SIMILARITY: Belongs to the GBP family.
 CC -----
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 CC -----
 CC EMBL; AJ007970; CAA07797.1; -;
 DR EMBL; AF077007; AAC98287.1; -;
 DR EMBL; AF109168; AAD39746.1; -;
 DR EMBL; BC011336; AAH11336.1; -;
 DR EMBL; BC032882; AAH32882.1; -;
 DR HSSP; P32455; 1DG3.
 DR MGD; MGI:102772; Gbp2.
 DR InterPro; IPR003191; GBP.
 DR Pfam; PF02263; GBP; 1.
 DR Pfam; PF02841; GBP C; 1.
 DR GTP-binding; Interferon induction; Lipoprotein; Multigene family;
 KW Prenylation.
 KM NP_BIND 45 52 GTP (By similarity).
 FT NP_BIND 97 101 GTP (By similarity).
 FT LIPID 586 586 S-geranylgeranyl cysteine.
 FT CONFLICT 163 163 V -> I (in Ref. 4).
 FT CONFLICT 246 246 S -> T (in Ref. 3).
 FT CONFLICT 381 381 E -> D (in Ref. 4; AAH11336).
 SQ SEQUENCE 589 AA; 66739 MW; 8E68B0A3BC5F3AE3 CRC64;
 Query Match 57.5%; Score 1750.5; DB 1; Length 589;
 Best Local Similarity 62.8%; Pred. No. 1.2e-80;
 Matches 349; Conservative 84; Mismatches 114; Indels 9; Gaps 2;
 QY 1 MALETHMSDPMCLIEFNFOELKVNQENLEILSAITQPVVVVAIVGLYRTGKSLYMNKLKAG 60
 Db 1 MASETHMSFPMCLIENTEAQLVINOEAURLILSAITQPVVVVAIVGLYRTGKSLYMNKLKAG 60
 QY 61 KNGKFSVASTVQSHTKGIWCVPHNPWNPHLTVLLDTEGLGDVEKADNKNDIQIFALAL 120
 Db 61 KTGFSLSGSTVQSHTKGIWMCVPHPKAGQTLVLLDTEGLDEVEKGDQNDQWCFALAV 120
 QY 121 LLSSTFVYNTVNVKIDQGAIDLHNVTELTDLLKARNSPDLDRVEDPADSAPFDLVWTL 180
 Db 121 LLSSTFIYNSIGTINQAMQDLHYVTELTDLIKSKSPDQSGVDSANFVGFFPTFWTL 180
 QY 181 RPFCLGLEIDGQIVTPDEYLENSLRPKQGSQDVQVQNFNLRCLCIQKFFPKKCFIFDLPA 240
 Db 181 RDFSLELVNGRPVTSDEYLEHSLTLKKGADKKTSFNEPRLCIRKFFPKKCFIFDRPA 240
 QY 241 HOKKLAQLETLTPDDELEPEFVQVQTEFCYSYIFSHSMTKTLPGLGMVNGSLKNLVLTYYN 300
 Db 241 QRKQSLKSLTLEBEELCGEFVQVQAEFTSYILSYSSVKTLGGIIVNGRPLKSLVQTVYG 300
 QY 301 AISSGDLPLCIENAVLALAQRENSAAVQKAIADHYDQMGQKQVQLPMETLQELLDLHRTSR 360
 Db 301 AINSGLPCWESAVLTLAGIENSAVQKAITHYEQMNQKIQMPETTLQELLDLHRTSR 360
 QY 361 EAIENVKMSFKVDVDSFOKELETLDDAKNDICKENLEASDYSALLKIDIFGLEEAV 420
 Db 361 EAIENVKMSFKVDVDSFOKELETLDDAKNDICKENLEASDYSALLKIDIFGLEEAV 420
 QY 421 KGIYSKPGGHNLFQIKTBTLLKAKYVREPRKGIQAEVLQKYLKSKSVSHAILQDQAL 480
 Db 421 KQITSPKGGYFLQMRQELKKYNQAPKGLAEAVLKQYFESKEDIVETLLKTDQSL 480
 QY 481 TETKXKKAQVKAQAEKAEQALAAIQRONQWQERLHQEVRQWEIAKQWLABQ 536
 Db 481 TETKXKKAQVKAQAEKAEQALAAIQRONQWQERLHQEVRQWEIAKQWLABQ 536

Db 481 TAAKEVEERTKAAAEAAANRELEKKQKEFFELMMQOKEKSYQEHVKKLTEKMDOKQL 540
Qy 537 LAEQQ-----KMQEQQ 547
Db 541 LAEQENIIAAKUREQE 556

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